



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 149782

TO: Daniel E Kolker  
Location: REM-4A54/4C70  
Art Unit: 1646  
Thursday, April 07, 2005

Case Serial Number: 10/626445

From: Barb O'Bryen  
Location: Biotech-Chem Library  
Remsen 1a69  
Phone: 571-272-2518

barbara.obryen@uspto.gov

### Search Notes

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10-626445

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 21:24:32 ; Search time 5404 Seconds  
(without alignments)  
10544.658 Million cell updates/sec

Title: US-10-626-445-5  
Perfect score: 1176  
Sequence: 1 atgcggagcttaacagtac.....accagtcagtcattcttga 1176

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_ats.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1176	100.0	1538	10	AF358859 Mus muscu
2	958.4	81.5	1593	10	AF358860 Rattus no
3	821.4	69.8	199837	10	AC131672 Mus muscu
4	686.6	58.4	1173	6	AR142850 Sequence
5	686.6	58.4	1173	6	AR391860 Sequence
6	686.6	58.4	1173	6	AX109119 Sequence
7	686.6	58.4	1173	6	AX139113 Sequence
8	686.6	58.4	1173	6	BD015847 Novel pol
9	686.6	58.4	1173	9	AF325356 Homo sapi
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12	686.6	58.4	1173	9	AY136745 Homo sapi
13	686.6	58.4	1173	9	AJ298292 Homo sapi
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15	686.6	58.4	1300	6	AX301229 Sequence
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33	442	37.6	193779	2	AP001327 Homo sapi
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35	283.8	24.1	522	6	AY561470 Gorilla g
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37	270.6	23.0	429	6	CQ727333 Sequence
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ALIGNMENTS

RESULT 1  
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LOCUS AF358859 1538 bp mRNA linear ROD 02-SEP-2001  
DEFINITION Mus musculus histamine H4 receptor mRNA, complete cds.  
ACCESSION AF358859  
VERSION AF358859.1 GI:15420534  
KEYWORDS Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1538)  
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Comparison of human, mouse, rat, and guinea pig histamine H4  
receptor suggests substantial species variation  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1538)  
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Direct Submission  
JOURNAL Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson  
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,  
CA 92121, USA

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ORIGIN

Query Match 100.0%; Score 1176; DB 10; Length 1538;  
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 1176; Conservative 0; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAGTCTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCATTT 60  
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QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTTTGG 420  
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QY 1141 CCAGCGCTGTCA CAGNACCAAGTCAGTATCTCTTGA 1176  
DB 1201 CCAGCGCTGTCA CAGNACCAAGTCAGTATCTCTTGA 1236

RESULT 2  
AF358860 1593 bp mRNA linear ROD 02-SEP-2001  
LOCUS Rattus norvegicus histamine H4 receptor mRNA, complete cds.  
DEFINITION AF358860  
ACCESSION AF358860.1 GI:15420536  
VERSION  
KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE  
ORGANISM Rattus norvegicus  
REFERENCE 1 (bases 1 to 1593)  
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1593)  
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Direct Submission  
JOURNAL Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA

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ORIGIN  
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Best Local Similarity 88.4%; Pred. No. 28-260;  
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGTGGAGTCTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCATTT 60  
DB 36 ATGTGGAGTCTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCATTT 95  
QY 61 TTAATGTCTTCATTTGGCTTTGCTATAATGGTAGGCAATGCTGTGTCACTTAGGCTTT 120  
DB 96 TTAATGTCTTCATTTGGCTTTGCTATAATGGTAGGCAATGCTGTGTCACTTAGGCTTT 155  
QY 121 GTGGTGGACAGAACTTACAGATCGAAGTAATATTTTCTTAATTTGGCTATTCTTCT 180  
DB 156 GTAGCAGACAGAACTTACAGATCGAAGTAATATTTTCTTAATTTGGCTATTCTTCT 215

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Db 396 CGTTATAGACACAGCACACTGGCATCTGAAAATTTGTGTCAAAATGGTGGCTGTTTGG 455
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Qy 1141 CCAGCGCTGTACAGAACCCAGTCTAGTATCTTCTTGA 1176
Db 1176 CCAGCGCTTTCACAGACCCAGTCTAGTATCTTCTTGA 1211
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## RESULT 3

AC131672/c 199837 bp DNA linear ROD 11-FEB-2004  
LOCUS Mus musculus chromosome UNK clone RP23-314021, complete sequence.  
DEFINITION

ACCESSION AC131672  
VERSION AC131672.3  
KEYWORDS GI:42517281  
SOURCE HTG.  
ORGANISM Mus musculus (house mouse)  
REFERENCE 1 (bases 1 to 199837)  
AUTHORS Wilson,R.K.  
TITLE The sequence of Mus musculus clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 199837)  
AUTHORS McPherson,J.D. and Waterston,R.H.  
TITLE Direct Submission  
JOURNAL Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park  
REFERENCE 3 (bases 1 to 199837)  
AUTHORS Wilson,R.K.  
TITLE Direct Submission  
JOURNAL Submitted (06-NOV-2003) Genome Sequencing Center, 4444 Forest Park  
REFERENCE 4 (bases 1 to 199837)  
AUTHORS Wilson,R.K.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-2004) Genome Sequencing Center, 4444 Forest Park  
COMMENT On Feb 11, 2004 this sequence version replaced gi:38194370.

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu  
Contact: submissions@wustl.edu  
----- Project Information -----  
Center project name: M\_BA0314021  
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FEATURES  
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## ORIGIN

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Qy 478 AGCACGAACACAAAGGACTGTGAGCTTGGCTTTGTTTACAGAGTGGTACATCCTCACCATT 537  
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Db 93030 ACAATGCTCTTGAATTCCTGCTTCTGTGTCATCTCTGTGGCTTATTTCAATGTACAGATT 92971  
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DEFINITION Sequence 1 from patent US 6613533.
ACCESSION AR391860
VERSION AR391860.1 GI:40115588
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monisma,F.J., Morse,K.L.,
Umland,S.P. and Wang,S.
TITLE Histamine receptor
JOURNAL Patent: US 6613533-A 1 02-SEP-2003;
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ORIGIN
Query Match 58.4%; Score 686.6; DB 6; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2.6e-183;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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Qy 481 ACGAACAACAAAGGACTGTAGCCTGGCTTTGTTACAGATGGTACATCTCTCACCATTACA 540
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Qy 721 CCTGGATGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCTCAGAAAGAGCAGC 780
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ACCESSION AX109119
VERSION AX109119.1 GI:13924093
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monisma,F.J., Morse,K.L.,
Umland,S. and Wang,S.
TITLE Histamine receptor
JOURNAL Patent: WO 0125432-A 1 12-APR-2001;
SCHERING CORPORATION (US)
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Best Local Similarity 75.1%; Pred. No. 2.6e-183;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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QY	361	TCATATAGGCTCAACACATCGGATCATGAAGATTGTTGCTCAAAATGTTGGTGG	420
Db	361	TCATATAGGCTCAACACATCGGATCATGAAGATTGTTGCTCAAAATGTTGGTGG	420
QY	421	ATACTGGCTTTCTTGTGTAATGCGGATGATTCGCTTCAGATTCCTTGGAGACAGC	480
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Db	835	TTCTCCCATCAGATCTGTAGCTCTTCCAAAGGAGACATGTTGAATGCTTACAGGC	894
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QY	961	TACTGTCTTCAATGCTGCTTCTCACTTACCCAGAGGAGGAGGAGGAGGAGGAGGAG	1020
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QY	1021	TGCTACAGATTCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1080
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LOCUS AX139113 1173 bp DNA linear PAT 30-MAY-2001  
DEFINITION Sequence 1 from Patent EP1096009.  
ACCESSION AX139113  
VERSION AX139113.1 GI:14274791  
KEYWORDS

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Peter, B. and O'Reilly, M.A. G-protein coupled receptor-like polypeptide Patent: EP 1096009-A 1 02-MAY-2001; Pfizer Limited (GB); PFIZER INC. (US)
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Best Local Similarity	75.1%; Pred. No. 2.6e-183;
Matches	886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
QY	1 ATGTGGAGTCTAAGTACTGCTGCTTGGCCAGCTGCTCAGCTCCCTTGGCATTT 60
Db	1 ATGCCAGATCTAATAGCAATCAATTTATCATAAGCACTGCTTACTTTAGCATTT 60
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Db	775	CTCATGTTTCTCAAGAACCAAGATGAATACAAATACAAATGCTTCAAAATGGGTCC	834
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DEFINITION	Novel polypeptide.		
ACCESSION	BD015847		
VERSION	BD015847.1	GI:22556984	
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Peter B. and Olaylee, M.A.		
TITLE	Novel polypeptide		
JOURNAL	Patent: JP 2001211889-A 1 07-AUG-2001;		
COMMENT	PFIZER INC		
	OS Homo sapiens (human)		
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Matches	886;	Conservative	0;	Mismatches	284;	Indels	9;	Gaps	2
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LOCUS AF329449 1173 bp mRNA linear PRI 29-APR-2001
DEFINITION Homo sapiens histamine receptor H4 mRNA, complete cds.
ACCESSION AF329449
VERSION AF329449.1 GI:13876643
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A.,
Anthes, J.C., Umland, S., Wan, Y., Hipkin, R.W., Gonsiorek, W., Shin, N.,
Gustafson, E.L., Glao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M.
and Monema, F.J. Jr.
Cloning and characterization of a novel human histamine receptor
J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)
PUBMED 21104636
JOURNAL J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)
MEDLINE 21104636
AUTHORS Monema, F.J. Jr., Wang, S., Behan, J., Laz, T.M., Greene, J. and
Bayne, M.
DIRECT SUBMISSION
SUBMITTED (15-DEC-2000) Human Genomics Research, Schering-Plough
Research Institute, 2015 Galloping Hill Rd., Kenilworth, NJ 07033,
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Query Match 58.4%; Score 686.6; DB 9; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2.6e-183;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
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AY008280
LOCUS AY008280 1173 bp mRNA linear PRI 15-MAR-2004
DEFINITION Homo sapiens histamine receptor H4 (H4) mRNA, complete cds.
ACCESSION AY008280
VERSION AY008280.1 GI:15822540
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1173)
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,
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Query Match	58.4%;	Score	686.6;	DB	9;	Length	1173;
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RESULT 13

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LOCUS Homo sapiens mRNA for histamine receptor H4 (HRH4 gene).

DEFINITION

ACCESSION AJ298292

VERSION AJ298292.1 GI:18152452

KEYWORDS histamine receptor H4; HRH4 gene.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS O'Reilly,M.A.

TITLE Identification of a histamine H4 receptor on human eosinophils - Role in eosinophil chemotaxis

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1173)

AUTHORS O'Reilly,M.A.

TITLE Direct Submission

JOURNAL Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer Ltd, Ramsgate Road, Sandwich, Kent, CT13 9NJ, UNITED KINGDOM

FEATURES

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Query Match 58.4%; Score 686.6; DB 9; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 2.6e-183;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
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DEFINITION Sequence 5 from Patent WO0200719.  
ACCESSION AX376577  
VERSION AX376577.1 GI:19170678  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Lin,D.C., Zhao,J., Chen,J.L. and Cutler,G.  
TITLE Novel receptors  
JOURNAL Patent: WO 0200719-A 5 03-JAN-2002;  
Tularik Inc. (US)

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ACCESSION AX301229
VERSION AX301229.1 GI:17382320
KEYWORDS Homo sapiens (human)
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## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Lind, P., Sehlitz, T., Vogeli, G. and Wood, L.S.

## AUTHORS

G protein-coupled receptors

## JOURNAL

Patent: WO 0185793-A 1 15-NOV-2001;

## FEATURES

PHARMACIA &amp; UPJOHN COMPANY (US)

## source

Location/Qualifiers

## ORIGIN

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Best Local Similarity 75.1%; Pred. No. 2.6e-183;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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Db 41 ATGCCAGATCTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTGTACITTTAGCAITTT 100

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Search completed: April 7, 2005, 00:31:11  
Job time : 5413 secs

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OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 19:47:57 ; Search time 729 Seconds  
(without alignments)  
9549.542 Million cell updates/sec

Title: US-10-626-445-5

Perfect score: 1176

Sequence: 1 atgtcggagttaacagttac.....accagtcagttatcttctga 1176

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870657 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1176	100.0	1176	6	AAI70981 Mouse his
2	1176	100.0	1538	12	ADO30257
3	958.4	81.5	1176	6	AAI70982 Rat hist
4	686.6	58.4	1173	3	AAA46023 Human G p
5	686.6	58.4	1173	3	AAAD01124 Human G p
6	686.6	58.4	1173	4	AAI70982 Human GPC
7	686.6	58.4	1173	5	AAI70982 Human GPC
8	686.6	58.4	1173	6	AAI70982 Human GPC
9	686.6	58.4	1173	6	AAI70982 Human GPC
10	686.6	58.4	1173	6	AAI70982 Human GPC
11	686.6	58.4	1173	8	AAI70982 Human GPC
12	686.6	58.4	1173	10	AAI70982 Human GPC
13	686.6	58.4	1173	10	AAI70982 Human GPC
14	686.6	58.4	1173	11	AAI70982 Human GPC
15	686.6	58.4	1173	12	AAI70982 Human GPC
16	686.6	58.4	1173	12	AAI70982 Human GPC
17	686.6	58.4	1173	12	AAI70982 Human GPC
18	686.6	58.4	1173	12	AAI70982 Human GPC
19	686.6	58.4	1266	6	ABK12959 DNA sequ
20	686.6	58.4	1300	6	ABA02496 Human G p

21	686.6	58.4	1312	4	AAH47911	Human G p
22	686.6	58.4	3689	8	ABZ42573	Human his
23	686.6	58.4	3689	12	ADO5719	Human his
24	686.6	58.4	3689	12	ADO29967	Human GPC
25	685.2	58.3	1170	9	AAI66009	Human H4
26	685	58.2	1227	4	AAI66009	Human GPR
27	685	58.2	1265	6	AAI66009	Human DNA
28	685	58.2	1265	9	AAI66009	Human H4
29	683.4	58.1	1173	6	AAI67750	Human his
30	613	52.1	1170	6	AAI70983	Guinea pi
31	505.8	43.0	1166	9	AAI70983	Human H4
32	436.6	37.1	1103	9	AAI70983	Human H4
33	271.6	23.1	1326	6	AAI70983	Human G-p
34	269	22.9	540	6	AAI70983	Human DNA
35	172.8	14.7	1239	2	AAI70983	G-protein
36	172.8	14.7	1239	3	AAI70983	Rat G-pro
37	172.8	14.7	2700	2	AAI70983	G-protein
38	172.8	14.7	2700	3	AAI70983	Rat G-pro
39	171.6	14.6	1311	9	AAI70983	Human H3
40	168.6	14.3	1203	9	AAI70983	Human H3
41	145.4	12.4	1338	12	AAI70983	Murine hi
42	145.4	12.4	18105	8	AAI70983	Mouse his
43	143.8	12.2	2483	12	AAI70983	Mouse GPC
44	143.2	12.2	1338	2	AAI70983	Rat musca
45	143.2	12.2	1953	3	AAI70983	Rat G-pro

## ALIGNMENTS

### RESULT 1

AAI70981  
ID AAI70981 standard; cDNA; 1176 BP.

XX AAI70981;

AC AAI70981;

XX 18-MAR-2002 (first entry)

DT Mouse histamine H4 receptor cDNA.

DE Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;

KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;

KW diagnosis; gene therapy; ss.

XX Mus musculus.

OS WO200192485-A1.

PN 06-DEC-2001.

PD 22-FEB-2001; 2001WO-US005914.

PF 31-MAY-2000; 2000US-0208260P.

XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Lovenberg T, Liu C;

XX WPI; 2002-114339/15.

XX P-ESDB; AAM50565.

XX New mammalian histamine H4 receptor proteins and polynucleotides encoding

PT the proteins, useful in gene therapy for treating diseases where it is

PT beneficial to elevate mammalian histamine H4 receptor activity.

XX Claim 4; Fig 5A; 92pp; English.

PS The present sequence is that of a cDNA clone encoding a murine histamine

CC receptor of the H4 subtype. The cDNA was isolated from a mouse spleen

CC cDNA library. It shows 72.8% homology to the human H4 receptor coding

CC region. The invention provides mammalian (human, mouse, rat and guinea

CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and

CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in



CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein H4 receptor. Such modulators may be  
 CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
 CC useful for diagnosing, treating or preventing asthma, allergy,  
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity  
 XX  
 SQ Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1176; DB 6; Length 1176;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGTCGGAGCTAAACAGTACTGGCATCTTGGCCACACAGCTGCTCAGGTCCCTTGGCATTT 60  
 DB 1 ATGTCGGAGCTAAACAGTACTGGCATCTTGGCCACACAGCTGCTCAGGTCCCTTGGCATTT 60  
 QY 61 TTAATGCTCTTCAATTCGCTTGTATATAATGGTAGGCAATGCTGTGTCATCTTACGCTTT 120  
 DB 61 TTAATGCTCTTCAATTCGCTTGTATATAATGGTAGGCAATGCTGTGTCATCTTACGCTTT 120  
 QY 121 GTGGTCGACAGAAACCTTAGACATCGAATTAATTTTCTTAATTTGGCTATTTCT 180  
 DB 121 GTGGTCGACAGAAACCTTAGACATCGAATTAATTTTCTTAATTTGGCTATTTCT 180  
 QY 181 GACTTCTCTGTTGGTTTGAATTTCCATTCCTGTACATCCCTCACGCTGTTGTTAACTGG 240  
 DB 181 GACTTCTCTGTTGGTTTGAATTTCCATTCCTGTACATCCCTCACGCTGTTGTTAACTGG 240  
 QY 241 AATTTTGGAGTGAATCTGCATGTTTGGCTCATCTACTGACTATCTTTGTGACCGCA 300  
 DB 241 AATTTTGGAGTGAATCTGCATGTTTGGCTCATCTACTGACTATCTTTGTGACCGCA 300  
 QY 301 TCTGCTTACATATTTGCTCATTAGTACGATCGATCAGTCACTGTTCAATGCTGTG 360  
 DB 301 TCTGCTTACATATTTGCTCATTAGTACGATCGATCAGTCACTGTTCAATGCTGTG 360  
 QY 361 TCTTATAGGCTCAACACACTGGCATCTGAAGATTTGCTCAAAATGGTGGCTGTTGG 420  
 DB 361 TCTTATAGGCTCAACACACTGGCATCTGAAGATTTGCTCAAAATGGTGGCTGTTGG 420  
 QY 421 ATACTGGCTTTCTTGGTAAATGCCGATGATTTCTGGCTTCAAGATTTCTTGGAGAACAGC 480  
 DB 421 ATACTGGCTTTCTTGGTAAATGCCGATGATTTCTGGCTTCAAGATTTCTTGGAGAACAGC 480  
 QY 481 ACGAACACAAAGGACTGTGAGCTGCTGCTGTTGTTACAGAGTGGTACATCTCACCATTACA 540  
 DB 481 ACGAACACAAAGGACTGTGAGCTGCTGCTGTTGTTACAGAGTGGTACATCTCACCATTACA 540  
 QY 541 ATGCTCTTGGAAATTCCTGCTTCTGTCATCTCTGCTGCTTATTTCAATGTACAGATTTAC 600  
 DB 541 ATGCTCTTGGAAATTCCTGCTTCTGTCATCTCTGCTGCTTATTTCAATGTACAGATTTAC 600  
 QY 601 TGGAGCCTGTGGAAGCGTATGGGCTCTCAGTAGGTGCTTACGATGCTGGATTTCTCACT 660  
 DB 601 TGGAGCCTGTGGAAGCGTATGGGCTCTCAGTAGGTGCTTACGATGCTGGATTTCTCACT 660  
 QY 661 ACCTCTTCAGTCTTTCAGGACACTTACACAGAGCTGGGCTGGCTTGCAGGACAGTAAT 720  
 DB 661 ACCTCTTCAGTCTTTCAGGACACTTACACAGAGCTGGGCTGGCTTGCAGGACAGTAAT 720  
 QY 721 CCTGGATTCGAAGAACTCAGCTGATCTCGTCACTCAGAAAGTCTCTCGAAGAAAGACAGC 780  
 DB 721 CCTGGATTCGAAGAACTCAGCTGATCTCGTCACTCAGAAAGTCTCTCGAAGAAAGACAGC 780  
 QY 781 ATCTCTGGTGTCTTAAAGGACTCAGTAAACAGCAGTATCACTGCTTCAAAAGTGGTTC 840  
 DB 781 ATCTCTGGTGTCTTAAAGGACTCAGTAAACAGCAGTATCACTGCTTCAAAAGTGGTTC 840

RESULT 2  
 AD030257

ID AD030257 standard; cDNA; 1538 BP.

AC AD030257;

DT 29-JUL-2004 (first entry)

XX Mouse GPCR HRH4 polynucleotide, SEQ ID NO:1360.

DE G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 XX transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;  
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
 KW kidney disorder; liver disorder; lung disorder; breast disorder;  
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; antianic;  
 KW cyostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
 KW viricide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
 KW murine; gene; ss.

XX Mus musculus.

OS WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

PR 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI; 2004-390329/36.

DR F-PSDB; ADO29497.

XX Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina



PT pectoris, Parkinson's disease.

PS Claim 151; SEQ ID NO 1360; 542bp; English.

XX The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridize to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR-encoding nucleic acid of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pcr\_sequences.

XX SEQ Sequence 1538 BP; 357 A; 362 C; 340 G; 479 T; 0 U; 0 Other;

Query Match		100.0%;	Score 1176;	DB 12;	Length 1538;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1176;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCTCCCTTGGCAATT	60		
Db	61	ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCTCCCTTGGCAATT	120		
Qy	61	TTAATGCTCTCAATTTGGCTTTGCTATATAGTAGGCAATGCTGGTCACTCTAGCCCTTT	120		
Db	121	TAAATGCTCTCAATTTGGCTTTGCTATATAGTAGGCAATGCTGGTCACTCTAGCCCTTT	180		
Qy	121	GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT	180		
Db	181	GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT	240		
Qy	181	GACTTCCTCGTGGTGTGATTTCCATTCCTCTGTACATCCCTCAGCTGTGTTAACTGG	240		
Db	241	GACTTCCTCGTGGTGTGATTTCCATTCCTCTGTACATCCCTCAGCTGTGTTAACTGG	300		
Qy	241	AATTTTGAAGTGGAAATCGCATGTTTGGCTCATCTAGCATATCTTTTGTGCAACCGCA	300		
Db	301	AATTTTGAAGTGGAAATCGCATGTTTGGCTCATCTAGCATATCTTTTGTGCAACCGCA	360		
Qy	301	TCTGTCTACAATATTGCTCTATTAGCTACGATCGATACCATCAGTCTCAAAATGCTGTG	360		
Db	361	TCTGTCTACAATATTGCTCTATTAGCTACGATCGATACCATCAGTCTCAAAATGCTGTG	420		
Qy	361	TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGCTGTGTTGG	420		
Db	421	TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGCTGTGTTGG	480		
Qy	421	ATATGCGCTTCTTGGTAAATGGCCGATGATCTTGGCTTCAGATCTTGGAGAACAGC	480		
Db	481	ATATGCGCTTCTTGGTAAATGGCCGATGATCTTGGCTTCAGATCTTGGAGAACAGC	540		

Qy	481	ACGAACACAAAGGACTGTGAGCTGGCTTTGTACAGAGTGGTATACATCTCCACCATTACA	540
Db	541	ACGAACACAAAGGACTGTGAGCTGGCTTTGTACAGAGTGGTATACATCTCCACCATTACA	600
Qy	541	ATGCTCTTTGGAAATTCCTGCTTCCTGTATCTCTGTGGCTTATTTCAATGTACAGATTTAC	600
Db	601	ATGCTCTTTGGAAATTCCTGCTTCCTGTATCTCTGTGGCTTATTTCAATGTACAGATTTAC	660
Qy	601	TGGAGCTGTGGAAGCGTAGGCTCTCTAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT	660
Db	661	TGGAGCTGTGGAAGCGTAGGCTCTCTAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT	720
Qy	661	ACCTCTTTCCAGTGTCTTCAAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT	720
Db	721	ACCTCTTTCCAGTGTCTTCAAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT	780
Qy	721	CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCGAAGAAAGAGCAGC	780
Db	781	CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCGAAGAAAGAGCAGC	840
Qy	781	ATCTGGTGTCTTAAAGGACTCACATGAACAGCAGTATCATCTGCCCTTCAAAAGTGGTTCC	840
Db	841	ATCTGGTGTCTTAAAGGACTCACATGAACAGCAGTATCATCTGCCCTTCAAAAGTGGTTCC	900
Qy	841	TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTAGCGCAGAGCTTCTCAGAGGC	900
Db	901	TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTAGCGCAGAGCTTCTCAGAGGC	960
Qy	901	AGGAAGCTAGCCAGGTCTACTGGCCATCTTCTGAGCGCTTTTGCATTTGCTGGGCTCCA	960
Db	961	AGGAAGCTAGCCAGGTCTACTGGCCATCTTCTGAGCGCTTTTGCATTTGCTGGGCTCCA	1020
Qy	961	TACTGTCTGTTCAAAATGCTCTTCACTTACCCAGAACGAGACGCCCAAAATCGGTG	1020
Db	1021	TACTGTCTGTTCAAAATGCTCTTCACTTACCCAGAACGAGACGCCCAAAATCGGTG	1080
Qy	1021	TGGTACAGCATTTGCTCTGGCTGCAATGGTTCATTTGTTTAAATCCCTTTCTGTAC	1080
Db	1081	TGGTACAGCATTTGCTCTGGCTGCAATGGTTCATTTGTTTAAATCCCTTTCTGTAC	1140
Qy	1081	CCTTTGTGTACAGGCGTTTCCAGAGCTTTTGTGGAAGATACCTTTGTGTGACAAAGCAA	1140
Db	1141	CCTTTGTGTACAGGCGTTTCCAGAGCTTTTGTGGAAGATACCTTTGTGTGACAAAGCAA	1200
Qy	1141	CCAGCGCTGTACAGAACCCAGTCAGTATCTTCTTGA	1176
Db	1201	CCAGCGCTGTACAGAACCCAGTCAGTATCTTCTTGA	1236

RESULT 3

AAI70982

ID AAI70982 standard; cDNA; 1176 BP.

XX

AC AAI70982;

XX

DT 18-MAR-2002 (first entry)

XX

DE Rat histamine H4 receptor cDNA.

XX

KW Histamine H4 receptor; rat; antiasthmatic; antiallergenic;

KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;

XX diagnosis; gene therapy; ss.

OS Rattus rattus.

XX

PN WO200192485-A1.

XX

PD 06-DEC-2001.

XX

PF 22-FEB-2001; 2001WO-US005914.

XX

PR 31-MAY-2000; 2000US-0208260P.

XX (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX Lovenberg T, Liu C;  
XX WPI; 2002-114339/15.  
XX P-PSDB; AAM50566.  
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
PT the proteins, useful in gene therapy for treating diseases where it is  
PT beneficial to elevate mammalian histamine H4 receptor activity.  
XX  
XX Claim 4; Fig 5C; 92pp; English.  
XX  
XX The present sequence is that of a cDNA clone encoding a rat histamine  
CC receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA  
CC library. It shows 72.5% homology to the human H4 receptor coding region.  
CC The invention provides mammalian (human, mouse, rat and guinea pig)  
CC histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
CC recombinant host cells that produce active recombinant protein. The  
CC pharmacology of known histamine ligands is demonstrated. Mammalian  
CC histamine H4 receptor may be used in gene therapy for the treatment of  
CC diseases where it is beneficial to elevate mammalian histamine H4  
CC receptor activity. Recombinant protein is useful for identifying  
CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
CC useful for diagnosing, treating or preventing asthma, allergy,  
CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
CC disorders of the neuroendocrine system, stress and spasticity  
XX  
XX Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other;  
Query Match 81.5%; Score 958.4; DB 6; Length 1176;  
Best Local Similarity 88.4%; Pred. No. 1.7e-289;  
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGTCGGAGTCTAACAGTACTGCGATCTTGGCCACAGCTGCTCAGCTCCCTTGGCATTT 60  
DB 1 ATGTCGGAGTCTAACGGCAGTACGCTTGGCCACTGACTGCTCAAGTCCCTTGGCATTT 60  
QY 61 TTAATGTCTTCATTTGCTTTGCTATATAAGTAGGCAATGCTGTGCTATCTTAGCCTTT 120  
DB 61 TTAATGTCTTCGTTGCTTTGCTATTAACGATAGGCAATGCTGTGCTATCTTAGCCTTT 120  
QY 121 GTGGTGAGCAAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTTCT 180  
DB 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTTCT 180  
QY 181 GACTTCTCTGCTGGGTTTGATTTCCATTCCTCTGTACATCCCTCACGTTGTTTAACTGG 240  
DB 181 GACTTCTCTGCTGGGTTGATCTCTCAATTCCTCTGTACATCCCTCACGCTGTTTAACTGG 240  
QY 241 AATTTTGGAGTGGAACTGTCATGTTTGGCTCATTAAGTACATCTTTGTGCACCGCA 300  
DB 241 AATTTTGGAGTGGAACTGTCATGTTTGGCTCATTAAGTACATCTTTGTGCACCGCA 300  
QY 301 TCTGTCTACAAATATGTCCTCATTAAGTACGATCGATACAGTCAGTTTCAAAATGCTGTG 360  
DB 301 TCGGTCTACAGTATGTCCTCATTAAGTACGATCGATACAGTCAGTTTCAAAACGCTGTG 360  
QY 361 TCTTATAGGCTCAACACACTGTCATGAAATGTTGCTCAAAATGTTGCTGTTTGG 420  
DB 361 CGTTATAGAGCAGACACACTGTCATGAAATGTTGCTCAAAATGTTGCTGTTTGG 420  
QY 421 ATACTGGCTTTCTTGGTAAATGCTGATGTTTGGCTCATTAAGTACATCTTTGGAAGACAGC 480  
DB 421 ATACTGGCTTTCTTGGTCAATGCTGATGTTTGGCTCATTAAGTACATCTTTGGAAGACAGC 480  
QY 481 ACCAAACAGAAAGTGTGAGCTGCTGTTTGTACAGAGTGGTACATCTTACCATTTACA 540  
DB 481 ACCAAACAGAGGAGTGGAGCTGCTGTTTGTACTGAGTGGTACATCTTCCGCAATTACA 540

QY 541 ATGCTCTTGGAAATCTCTGCTTCTCTGTCATCTCTGTGGCTTATTTCAATGTCAGATTAC 600  
DB 541 GCATTTCTTGGAAATCTCTGCTTCTCTGTCATCTCTGTGGCTTATTTCAATGTCAGATTAC 600  
QY 601 TGGAGCCTGTGGAAGCGTAGGCTCTCAGTAGGTGCTTCCAGCATGCTGCTGCTTCCACT 660  
DB 601 TGGAGCCTGTGGAAGCGTAGGCTCTCAGTAGGTGCTTCCAGCATGCTGCTGCTTCCACT 660  
QY 661 ACCTCTTCCAGTCTTCCAGGACACTTACACAGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
DB 661 ACCTCTTCCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
QY 721 CTTGATTCAGGAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
DB 721 CTTGATTCAGGAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
QY 781 ATCTCTGCTGCTTCTTAAAGTCTCAGTAAACAGCAGTATCAGTCTTCCAAAGTGGTTC 840  
DB 781 CTCTCTGCTGCTTCTTAAAGTCTCAGTAAACAGCAGTATCAGTCTTCCAAAGTGGTTC 840  
QY 841 TTCTGCGCATCGAAGTGCAGGCTTCCGCAAGGAGTACGAGAGCTTCTCAGAGGC 900  
DB 841 TTCTGCGCATCGAAGTGCAGGCTTCCGCAAGGAGTACGAGAGCTTCTCAGAGGC 900  
QY 901 AGAAGCTAGCCAGGCTCAGTGGCCATCTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960  
DB 901 AGAAGCTAGCCAGGCTCAGTGGCTTCTCAGAGAGAGCAGTGGAGCTTCTCAGAGGC 960  
QY 961 TACTGTCTTCCAAATTTGCTTCACTTACCAGAACCGAAGCGCCCAAAATCGGTG 1020  
DB 961 TATTGCTCTTCCAAATTTGCTTCACTTACCAGAACCGAAGCGCCCAAAATCGAT 1020  
QY 1021 TGGTACAGCATTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
DB 1021 TGGTACAGCATTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
QY 1081 CTTTGTGTCCAGGCGTTTCCAGAAAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140  
DB 1081 CTTTGTGTCCAGGCGTTTCCAGAAAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140  
QY 1141 CCAGCGCTGTCTACAGAACCCAGTCACTTCTTTGA 1176  
DB 1141 CCAGCACCTTTCACAGACCCAGTCACTTCTTTGA 1176  
RESULT 4  
AAA46023  
ID AAA46023 standard; cDNA; 1173 BP.  
XX  
AC AAA46023;  
XX  
DT 22-AUG-2000 (first entry)  
XX  
DE Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13.  
XX  
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;  
KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;  
KW SB.  
OS Homo sapiens.  
XX  
XX WO200022131-A2.  
PN  
XX 20-APR-2000.  
PD  
XX  
PF 13-OCT-1999; 99WO-US024065.  
XX  
XX 13-OCT-1998; 98US-00170496.  
PR 12-NOV-1998; 98US-0108029P.  
PR 20-NOV-1998; 98US-0109213P.  
PR 27-NOV-1998; 98US-0110060P.  
PR 16-FEB-1999; 99US-0120416P.  
PR 26-FEB-1999; 99US-0121852P.

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PR 12-MAR-1999; 99US-0123944P.
PR 12-MAR-1999; 99US-0123945P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123948P.
PR 12-MAR-1999; 99US-0123949P.
PR 12-MAR-1999; 99US-0123951P.
PR 12-MAR-1999; 99US-0123951P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 28-MAY-1999; 99US-0137567P.
PR 29-JUN-1999; 99US-0141448P.
PR 27-AUG-1999; 99US-0151114P.
PR 03-SEP-1999; 99US-0152524P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 12-OCT-1999; 99US-00417044.
XX
PA (AREN-) ARENA PHARM INC.
XX
XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX
XX WPI; 2000-317986/27.
DR P-PSDB; AAB02831.
XX
XX Non-endogenous, human G protein-coupled receptors for screening receptor,
PT inverse or partial agonists useful as therapeutic agents.
XX
XX Example 1; Page 88-89; 187pp; English.
XX
XX The present invention describes transmembrane receptors, preferably human
CC G protein coupled receptors (GPCR), for which the endogenous ligand is
CC unknown (orphan GPCR receptors). More specifically the present invention
CC relates to non-endogenous, constitutively activated versions of a human
CC GPCR. These non-endogenous human GPCRs can be useful for the direct
CC identification of candidate compounds as receptors agonists, inverse
CC agonists or partial agonists for use as pharmaceutical agents. AHA46017
CC to AHA46126 and AAB02825 to AAB02859 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
XX
XX Query Match 58.4%; Score 686.6; DB 3; Length 1173;
XX Best Local Similarity 75.1%; Pred. No. 3.4e-204;
XX Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
XX
XX 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGTCCCTTGSCATTT 60
DB 1 ATGCAGATACATAATAGCACAATCAATTTATCATCAATGACCTGCTGTTAGCATTT 60
XX
XX 61 TTAATGCTCTCATTTGGCTTTGCTATATAATGTTAGSCAAATGCTGTGGTCACTTAGCCCTTT 120
DB 61 TTTATGCTCTTAGTAGCTTTTGCTATATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120
XX
XX 121 GTGTGGACGAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
DB 121 GTGTGGACGAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
XX
XX 181 GACTTCTCTGTTGGTGTTCATTTCCATTCCTCTGTACATCCCTCAGCTGTGTTAACTGG 240
DB 181 GACTTCTCTGTTGGTGTTCATTTCCATTCCTCTGTACATCCCTCAGCTGTGTTAACTGG 240
XX
XX 241 AATTTTGGAGTGGAACTGCAATGCTTTTGGCTCATTTACTGACTATCTTTTGTGACCGCA 300
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Db 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
Qy 301 TCTGTCTACAATATTTGCTCCTCATTAGCTACGATCCATCCAGCTAGTTTCAATGCTGTG 360
Db 301 TCTGTATATAACATTTGCTCCTCATCAGCTATGATCATACCTGCTAGTCTCAATGCTGTG 360
Qy 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAATGGTGGCTGTTGG 420
Db 361 TCTTATAGAACTCAACATACTGGGCTCTTGAAGATTGTTACTCTGATGGTGGCCGTTGG 420
Qy 421 ATACTGGCTTTCTTGGTAATGGCCCGATGATTCTGGCTTCAGATTCCTTGGAAAGACAGC 480
Db 421 GTGCTGGCTTTCTTAGTGAATGGGCCAATGATTCTAGTTTTCAGAGCTCTTGGAAAGA- 476
Qy 481 ACGAACACAAAGGACTGTGAGCCTGGCTTGTGTTACAGAGTGTGATCATCTCACCAATTACA 540
Db 477 --TGAGGTAGTGAATGGAACCTGGATTTTTTTCGGAATGGTATCATCTTGCCTCATCA 534
Qy 541 ATGCTCTTTGGAATTCCTGCTTCTGTCTATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600
Db 535 TCATTTCTTGGAAATTCGTGATCCAGTCACTTAGTTCGCTTATTTCAACATGAATATTTAT 594
Qy 601 TGGAGCCTGTGGAAAGCTGAGGCTCTCAGTAGTGGCCCTAGCCATGCTGGATTTCCACT 660
Db 595 TGGAGCCTGTGGAAAGCTGATCATCTCAGTAGTGGCCCAAGCCATCTCTGGACTGCTGCT 654
Qy 661 ACCTCTTCCAGTCTTTCAGGACACTTACAGAGCTGGGGTGGCTTGCAGGACAGTAAT 720
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714
Qy 721 CCTGATTTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCTCGAAGAAAGACAGC 780
Db 715 TCTGCATCGACAGAGTTTCTGTCATCTTTCATTTCAGAGACACAGAGAGAAAGTAGT 774
Qy 781 ATCTGTGTCTTAAAGGACTCACAATGAACAGCAGTATCATGCTTCAAGTGGGTGCC 840
Db 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAATGGGTGCC 834
Qy 841 TTCTGGCATCGGAAGTGCAGCGCTTCGCCAAGGGAGTACGCAGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTTCTGTAGCTTTCACCAAGGGAAACATGTTGAACCTGCTTAGAGCC 894
Qy 901 AGGAAGCTAGCCAGCTCACTGGCCATCTCTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTTGTGCTGGCTCCA 954
Qy 961 TACTGTCTGTTCAAAATTTGCTTTCAACTTTACCCAGAACGGAACGCCCAAAATCGGTG 1020
Db 955 TATTCTCTGTTCAAAATTTGCTTTTCAATTTTATTTCTCAGCAACAGGCTCTTAAATCAGTT 1014
Qy 1021 TGGTACAGCATTTGCTTCTGGCTGCAATGGTTCAATTTGTTGTTTAAATCCCTTCTGTAC 1080
Db 1015 TGTATAGAAATTTGCAATTTTGGCTTTCAGTGGTTCAATTTCTTTGTCAATCTCTTTGTAT 1074
Qy 1081 CTTTGTGTACAGCGCTTTCCAGAGGCTTTCTGGAAGATCTTTGTTGTCAGCAAAAGCAA 1140
Db 1075 CCATTGTGTACAGCGCTTTCAAAAGGCTTTCTTGAANAATATTTTGTATATAAAGCAA 1134
Qy 1141 CCAGCGTGTACAGAAC---CAGTCAATATCTTTTGA 1176
Db 1135 CCTCTACCATCACAAACACAGTCGGTCAATCTCTCTTAA 1173
```

## RESULT 5

AAD01124

ID AAD01124 standard; cdna; 1173 BP.

XX AC AAD01124;

XX DT 02-NOV-2000 (first entry)

XX DE Human orphan G protein-coupled receptor hrUP7 cdna.

XX Human; orphan G protein-coupled receptor; GPCR; hrUP7; drug screening;  
 KW transmembrane receptor; signal cascade; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 1. .1173  
 FT CDS /tag= a  
 FT /product= "hrUP7"  
 FT /note= "Human orphan G protein-coupled receptor"  
 PN W0200031258-A2.  
 XX 02-JUN-2000.  
 XX 13-OCT-1999; 99NO-US023687.  
 XX 20-NOV-1998; 99US-0109213P.  
 PR 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 28-MAY-1999; 99US-0123949P.  
 PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136439P.  
 PR 28-MAY-1999; 99US-0136567P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 29-JUN-1999; 99US-0141448P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156633P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 29-SEP-1999; 99US-0156853P.  
 PR 01-OCT-1999; 99US-0157280P.  
 PR 01-OCT-1999; 99US-0157281P.  
 PR 01-OCT-1999; 99US-0157282P.  
 PR 01-OCT-1999; 99US-0157293P.  
 PR 01-OCT-1999; 99US-0157294P.  
 PR 12-OCT-1999; 99US-00416760.  
 PR 12-OCT-1999; 99US-00417044.  
 XX (AREN-) ARENA PHARM INC.  
 XX Chen R, Dang HT, Liaw CW, Lin I;  
 DR WPI; 2000-400068/34.  
 DR P-PSDB; AAY71297.  
 PT Novel human orphan G protein-coupled receptors and the encoding cDNAs for  
 PT use in the identification of G protein-coupled receptor agonists.  
 XX Claim 25; Page 59; 102pp; English.  
 XX The present sequence is a cDNA encoding hrUP7, an endogenous human orphan  
 CC G protein-coupled receptor (GPCR). The full length hrUP7 cDNA was cloned  
 CC by RT-PCR using human peripheral leucocyte cDNA as template. The orphan  
 CC GPCR of the invention, like all GPCRs has seven transmembrane alpha  
 CC helices with an extracellular N-terminus and an intracellular C-terminus.  
 CC However, no endogenous ligands has yet been identified for the proteins  
 CC of the invention. The orphan GPCRs may be used in the identification of  
 CC their endogenous ligands and to screen potential GPCR agonists and  
 CC antagonists for use as pharmaceutical agents. The proteins may also be  
 CC used in the study of GPCR-mediated signalling cascades, and to elucidate  
 CC their precise role in normal and diseased human conditions. Nucleic acid  
 CC encoding human orphan GPCRs may be used for tissue localisation  
 CC expression analysis to provide information about their function in  
 CC healthy and pathological states  
 XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 Query Match 58.4%; Score 686.6; DB 3; Length 1173;  
 Best Local Similarity 75.1%; Pred. No. 3.4e-204;

Matches	886;	Conservative	0;	Mismatches	284;	Indels	9;	Gaps	2;
QY	1	ATGTCGGAGTCTAA	CAGTACTGGCATCTT	GCACACAGCTGCT	CAGTCCCTTGGCATTT	60			
DB	1	ATGCCAGATAC	TAATAGCACAAATCA	ATTATCACTAAGCAC	CTCGTGTACTTTAGCATTT	60			
QY	61	TTAAATGCTCTT	CAATTTGGCCCTT	TGCTATTAATGGT	AGCAATGCTGTGCTCATCTTAGCCTTT	120			
DB	61	TTTATGTCCT	TAGTAGCTTTT	GTCTATTAATGCT	TAGGAATGCTTTGGTCATTTAGCTTT	120			
QY	121	GTGGTGACAGAA	ACCTTAGACATCG	AAATAATATTTT	TTCTTAATTTGGCTATTCT	180			
DB	121	GTGGTGACAAAA	ACCTTAGACATCG	AAATAATATTTT	TTCTTAATTTGGCTATTCT	180			
QY	181	GACTTCCTCGT	GGTTGGATTTT	CCATTCCTCTG	TACATCCCTCACGCTGTTTAACTGG	240			
DB	181	GACTTCCTTGT	GGGTGTGATCT	CCATTCCTCTG	TACATCCCTCACGCTGTTTAACTGG	240			
QY	241	AATTTTGGAA	TGGAATCTG	CATGTTTGGCT	CATTACTGACTATCTTTTGTGCACGCA	300			
DB	241	GATTTTGGAA	TGGAATCTG	TAATTTGGCT	CACACTGACTATCTGTTAATGACGCA	300			
QY	301	TCGTCTACA	ATATTGTCCT	CAATAGTACG	ATCGATACAGTTCAGTTTCAAAATGCTGTG	360			
DB	301	TCGTATATA	TAACATTTG	TCTCATGAT	CGATACGTCAGTCTCAAAATGCTGTG	360			
QY	361	TCCTATAGG	CTCAACACACT	GGCATGATGA	AGATTTGTTGCTCAAAATGCTGTGTTGG	420			
DB	361	TCCTATAGA	AACTCAACATA	CTGGGTCTTGA	AGATTTGTTGCTCAAAATGCTGTGTTGG	420			
QY	421	ATACTGGCT	TTCTTGGTAA	TGGCCGATG	ATTTGGCTTCAGATTTCTTTGGAAAGACAGC	480			
DB	421	GTGCTGGCT	TTCTTAGTGA	TGGCCCAATG	ATTTAGATTTTCAAGAGTCTTTGGAAAGG	476			
QY	481	ACGAACA	CAAAAGGACT	GTGAGCTGTG	CTGCTTTGTTTACAGAGTGTGTACATCTCACCATTACA	540			
DB	477	--TGAAG	GTAGTGAAT	TGAACCTG	GAATTTTTCGGAATGGTGTACATCTTGCATCACA	534			
QY	541	ATGCTCTT	GGAAATTCCT	CTGCTCACT	CTGTGGCTTATTTCAATCTACAGATTTAC	600			
DB	535	TCATTCTT	GGAAATTCGT	GATCCAGT	CACTCTTAGTCGCTTATTTCAACATGAATATTTAT	594			
QY	601	TGGAGCT	GTGGAAGCGT	AGGGCTCT	CAGTAGTGCTCTAGCATCTCTGAGATTTCTCCACT	660			
DB	595	TGAGGCT	GTGGAAGCGT	GATCATCT	CAGTAGTGCTCAAAAGCCATCTCTGAGTACTGCT	654			
QY	661	ACCTCTT	CCAGTGTTC	AGGACACTT	ACAGAGCTGGGGTGGCTTTCAGGACAAATAT	720			
DB	655	GTCTCTT	CCAAACAT	CTGTGGAC	CACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT	714			
QY	721	CCTGGAT	TGAAGGAAT	CAGTGCAT	CTCGTCACTCAGAAAGTCTCTCGAAGAGACAGC	780			
DB	715	CTGCAT	CGACAGAAGT	TCTGCATCT	CAATTCAGAGAGACAGAGGAGAAGAGTAGT	774			
QY	781	ATCTCTG	TGCTCTT	AAGGACT	CACATGAACAGCAGTATCACTGCCCTTCAAAAGTGGTTC	840			
DB	775	CTCATG	TTTTCTC	CAAGAACCA	AGATGATGAATACATTTGCTTCCAAATGGGTTC	834			
QY	841	TTCTGCG	CGATCGGAA	AGTACAGG	CTTCCGCAAGGAGTACGACAGCTTCTCAGAGGC	900			
DB	835	TTCTCCA	ATCAGAT	TCGTAGCT	CTTCAACAAAGGGAACATGTTGAACTGTCTTAGAGCC	894			
QY	901	AGGAGCT	AGGAGGCT	CACTGGCC	ATCTTCTGAGCGCTTTTGGCAATTTGCTGGGCTCCA	960			
DB	895	AGGAGAT	TAGCAAGT	CACTGGCC	ATCTTCTAGGGGTTTTTGTCTGTTTGTGGGCTCCA	954			
QY	961	TACTGTCT	TTTCAAA	TGCTCTT	CAACTTAACTTAACTCCAGAACGCGCCCAAAATCGGTG	1020			
DB	955	TATTTCT	CTTTTCA	AAATGTC	CTTTTCAATTTTCTCAGCAACAGGCTCTTAAATCAGTT	1014			
QY	1021	TGGTACAG	CAATTCCT	TTGGCTG	CAATTTGTTTAACTCCCTTTTCTGTAC	1080			
DB	1015	TGGTATAGA	AAATTTG	CAATTTT	GGCTTCAATTTCTTGTCAATCTCTCTTTGTAT	1074			

QY 1081 CTTTGTGTCTCAGCGTTTCCAGAGGCTTTCTGGAAGATACATTTGTGTGCAAAAGCAA 1140  
 |||||  
 Db 1075 CCAATGTGTCAAGCGCTTTCAAAGGCTTTCTTGAATAATTTTGTATATAAAGCAA 1134  
 |||||  
 QY 1141 CCAGCGCTGTACAGAAC---CAGTCAGTATCTTCTTGA 1176  
 |||||  
 Db 1135 CCTCTACCATCAACACAGTCGCGTCAATCTTCTTAA 1173  
 |||||

RESULT 6

AAF83203  
 ID AAF83203 standard; cDNA; 1173 BP.  
 AC AAF83203;  
 XX  
 DT 09-JUL-2001 (first entry)  
 XX  
 DE Human GPCR-like polypeptide, PFI-013 encoding cDNA.

XX G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;  
 KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;  
 KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;  
 KW signal transduction; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..1173

XX /tag= a

XX /product= "PFI-013"

XX EP1096009-A1.

XX 02-MAY-2001.

XX 24-OCT-2000; 2000EP-00309364.

XX 29-OCT-1999; 99GB-00025641.

XX 20-APR-2000; 2000GB-00009973.

XX (PFI-013) PFIZER LTD.

XX (PFI-013) PFIZER INC.

XX Peter B. O'Reilly MA;

XX WPI; 2001-309854/33.

XX P-PSDB; AAB62445.

XX New G-protein coupled receptor-like polypeptide, polynucleotide for  
 PT screening drug candidates for treating diseases associated with signal  
 PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.  
 XX

PS Claim 1; Page 43; 66pp; English.

XX This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor  
 CC (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be  
 CC expressed by standard recombinant methodology. Antibodies and modulators  
 CC of PFI-013 are useful in the manufacture of a medicament for treating  
 CC allergic disorder, including extrinsic asthma, immunological disorders,  
 CC such as intrinsic asthma, vasculitic granulomatous disease, interstitial  
 CC and other pulmonary disease, including chronic obstructive pulmonary  
 CC disease (COPD), infectious, inflammatory disease, such as inflammatory  
 CC bowel disease and neoplastic and myeloproliferative diseases. They are  
 CC also useful for treating obesity, diabetes, metabolic, neurological  
 CC diseases, psychotherapeutics, urogenital disease, reproduction and sexual  
 CC medicine, inflammation, cancer, tissue repair, dermatology, photosensitizing,  
 CC skin pigmentation, osteoporosis, cardiovascular, gastrointestinal  
 CC diseases, allergy and respiratory disease, sensory organ disorders, sleep  
 CC disorders and hair loss. The PFI-013 protein and nucleic acid are useful  
 CC in the diagnosis and treatment of the above conditions and also for  
 CC screening drug candidates for the treatment of diseases associated with  
 CC signal transduction. The antibodies are also useful for enrichment of

CC eosinophils from mammalian, especially human blood and for detecting the  
 CC protein in biological samples  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 4; Length 1173;  
 Best Local Similarity 75.1%; Pred. No. 3.4e-204;  
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGAGTCTAAACAGTACTGCGATCTTGCCACAGCTGCTCAGCTCCCTTGGCATTTT 60  
 |||||  
 Db 1 ATGCCAGATCTAATAGCACAATCAATTTATCATCTAGCACTCGTGTACTTTAGCATTT 60  
 |||||  
 QY 61 TTAATGCTCTTCAATTTGCTTTGCTATATATGTTAGTCAATGCTGTGGTCTTCTTCTT 120  
 |||||  
 Db 61 TTTATGCTCTTGTAGTCTTTTGTCTATATGCTAGGAATGCTTTGGTCTTCTTCTTCTT 120  
 |||||  
 QY 121 GTGTGGACAGAAACCTTAGACATCGAAGTAAATTTTCTTCTTCTTCTTCTTCTTCTT 180  
 |||||  
 Db 121 GTGTGGACAGAAACCTTAGACATCGAAGTAAATTTTCTTCTTCTTCTTCTTCTTCTT 180  
 |||||  
 QY 181 GACTTCTCGTGGGTTGATTTCCATCTCTGTACATCCCTCAGCTGTGTTTAACTGG 240  
 |||||  
 Db 181 GACTTCTTGTGGGTGATCTCCATCTCTTGTACATCCCTCAGCTGTGTTTAACTGG 240  
 |||||  
 QY 241 AATTTTGGAGTGAATCTGCATGTTTTGGCTCATTTACTGACTATCTTTTGTGACCGCA 300  
 |||||  
 Db 241 GATTTTGGAGAGGAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300  
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 QY 301 TCTGTCTACAATATTTGCTCTCATTTAGCTACGATGATACAGTCAATGCTGTTT 360  
 |||||  
 Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATGATACCTCTCAGTCTCAATGCTG 360  
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 QY 361 TCTTATAGGCTCAACACACGTCATCATGAAGATTGTTGCTCAAAATGCTGCTTTGG 420  
 |||||  
 Db 361 TCTTATAGAACTCAACATACATCTGGGCTCTTGAAGATTGTTACTCTGATGCTGGCCGTTGG 420  
 |||||  
 QY 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTCTTTGGAAGAACAGC 480  
 |||||  
 Db 421 GTGCTGGCTTTCTTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGTCTTTGGNAGA --- 476  
 |||||  
 QY 481 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCTCACCACATTA 540  
 |||||  
 Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTTGCCATCACA 534  
 |||||  
 QY 541 ATGCTCTTGGAAATTCCTGCTTCTCATCTCTGCTGCTTATTTCAATGTACAGATTTAC 600  
 |||||  
 Db 535 TCATTTCTTGGAAATTCGTTGATCCAGTCACTTTAGTCGCTTATTTCAACATGAATATTTAT 594  
 |||||  
 QY 601 TGGAGCCTGTGGAAGCCTAGGGCTCTCAGTAGGTGCTTCCATGCTGCTGCTTCTTCCACT 660  
 |||||  
 Db 595 TGGAGCCTGTGGAAGCCTGATCATCTCAGTAGGTGCTTCCAAAGCCATCTTGGAGTCTGCT 654  
 |||||  
 QY 661 ACCTCTTCCAGTCTTCCAGGACATTTACAGAGCTGGGGTGGCTTTCAGAGCAAGTAAAT 720  
 |||||  
 Db 655 GTCTCTTCCAACATCTGTGGACATCTCATTAGAGGTAGACTATCTTCAAGAGAGATCTCTT 714  
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 QY 721 CCTGGATTGAGGAATCAGCTGCTGCTCCTGCTCAGAAAGTCTCAGAAAGAGAGCAGC 780  
 |||||  
 Db 715 TCTGCATCGACAGAAATTCCTGCTGCTTCTTCAATTCAGAGAGACAGAGAGAGAGTAGT 774  
 |||||  
 QY 781 ATCTCTGTGCTTCTTAAAGACTCACATGAACAGCAGTATCACTGCTTCTTCAAAAGTGGTTC 840  
 |||||  
 Db 775 CTCAATGTTTCTTCAAGAACCAAGATGANTAGCATACATTTGCTTCAAAATGGTTC 834  
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 QY 841 TTCTGGCGATCGGAAAGTGCAGCGCTTTCGCAAGAGGAGTACGAGAGCTTCTCAGAGGC 900  
 |||||  
 Db 835 TTCTCCCAATCAGATTTCTGTAGCTCTTCAACAAAGGGAACATGTTGAACCTGCTTAGAGCC 894  
 |||||  
 QY 901 AGGAAGTACCGAGTCACTGGCCATCTTCTGAGCGCTTTTTCGCAATTTGCTGGGCTCCA 960  
 |||||  
 Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTTCTTAGGGGTTTTTGTGTTTCTGGGCTCCA 954  
 |||||







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QY 421 ATACTGGCTTTCTTGTGTAATGCCCGATGATTCTGGCTTCAGATCTTTGGGAAGACAGC 480
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 421 GTCTGGCTTCTTAGTGAATGGCCAAATGATTCTAGTTTCAGAGTCTTGGAAAGG- - - 476
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 ACGAACACAAAGGACTGTGAGCCCTGCTTTTGTACAGAGTGGTACATCCTCACCATTACA 540
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 477 - -TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTGCATACA 534
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 541 ATGCTCTTGAATTCCTGCTTCTGTCTCACTCTGTGCTTATTTCAATGTACAGATTAC 600
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 535 TCATCTTGGAAATTCGTGATCCAGTCCATCTTAGTGCCTTATTTCAACATGAAATATTAT 594
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 601 TGCAGCTGTGGAAGCTGAGGCTCTCAGTAGTGCCTAGCCATGCTGGATTCTCACT 660
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 595 TGAAGCTGTGGAAGGCTGATCATCTCAGTAGTGCCTAGCCATCCTGACTGCT 654
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 661 ACCTCTTCCAGTCTTCAGGACACTTACACAGAGCTGGGTGCTTGCAGGACCAAGTAAT 720
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 721 CTGGAATGGAAGAACAGTGCATCTCGTCACTCAGAAAGTCTCGAAGAAAGACAGC 780
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 715 TCTGCAATCGACAGAGTCTCTGATCCTTTTCAATTCAGAGAGACAGAGGAGAAAGTAGT 774
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 781 ATCTGTGTCTTAAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAGTGGTTC 840
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 775 CTATGTTTTCTCAAGAACAGATGAATAGCAATCAATTCCTTCCAAATGGGTTC 834
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 841 TTCTGGCATCGGAAAGTGCAGCGCTTCGCAAGGGAGTACGACAGAGCTTCTCAGAGGC 900
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 835 TTCTCCCAATCAGATTCTGTAGCTTTCACCAAGGGACATGTTGAAGTCTTAGAGCC 894
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 901 AGAAGCTAGCAGGTACATGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGTCCA 960
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTCTGTGCTGGGTCCA 954
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 961 TACTGTCTGTCAAAATGCTTCAACTTACCACAGAACGCAAGCCCAATCGGTG 1020
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 955 TATCTCTGTTCAAATGTCCTTCAATTTATTTCTCAGCAAGCTCTCAATCAGTT 1014
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1021 TGGTACAGCATTCCTTCTGGCTGCAATGGTTCAATTCGTTTGTAAATCCCTTTCTGTAC 1080
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1015 TGGTATAGATTGCAATTTTGGCTTCAGTGTTCAATTCCTTCTCAATCCTCTTTGTAT 1074
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1081 CCTTTGTGTACAGGCGTTTCCAGAGGCTTCTGGAAGATCTTGTGTGACAAAGCAA 1140
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1075 CCATTGTGTACAGGCGTTTCAAAAGGCTTCTTGAATAATTTTGTATAAAAGCAA 1134
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1141 CCAGCGCTGTACAGAAC- - -CAGTCAGTATCTTTGA 1176
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1135 CCTTACCATCACACAGCTCGTCAATCTTCTTAA 1173
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

## RESULT 9

ABQ78739

ID ABQ78739 standard; DNA; 1173 BP.

XX AC ABQ78739;

XX 05-DEC-2002 (first entry)

DE Nucleotide sequence of human histamine receptor.

XX Human; histamine receptor; receptor; inflammation; asthma; allergy;  
KW atopic dermatitis; stroke; myocardial infection; migraine;  
KW chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;  
KW multiple sclerosis; inflammatory bowel disease; psoriasis;  
KW intracellular second messenger pathway; cellular growth rate;  
KW hormone secretion; gene; ss.

XX Homo sapiens.

XX Location/Qualifiers

PH key

CDS 1. .1173  
/\*tag= a  
/product= "histamine receptor"

US2002098539-A1.

25-JUL-2002.

19-MAR-2001; 2001US-00812216.

07-OCT-1999; 99US-00414010.

(BEHA/) BEHAN J X.

(HEDR/) HEDRICK J A.

(LAZI/) LAZ T M.

(MONS/) MONSMA F J.

(MORS/) MORSE K L.

(UMLA/) UMLAND S P.

(WANG/) WANG S.

Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;  
Wang S;

WPI; 2002-673827/72.

P-PSDB; ABB78276.

Novel mammalian histamine receptor polypeptide useful for identifying  
agonist or antagonist for treating diseases such as inflammation, asthma,  
stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.  
Example 1; Page 15-16; 21pp; English.

The present sequence encodes a human histamine receptor. The polypeptide  
is useful for identifying an agonist or antagonist of a mammalian  
histamine receptor. It is useful as an antigen to elicit the production  
of antibodies. The histamine receptor polypeptide and polynucleotide are  
useful in the treatment and management of diseases such as inflammation,  
asthma, allergy, atopic dermatitis, stroke, myocardial infection,  
migraine, chronic obstructive pulmonary disease (COPD), rheumatoid  
arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.  
They are also useful for modulating intracellular second messenger  
pathway activated through histamine receptors (cyclic-AMP, calcium,  
inositol phosphate and mitogen activated protein (MAP kinase), changes  
in cellular growth rate, secretion of hormones, receptor-stimulated Ca<sup>2+</sup>  
mobilization, mitogenic effects, etc

SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 6; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 3.4e-204;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTTGCCACCAGCTGCTCAGTCCCTTTGGCATTT 60

Db 1 ATGCCAGATACTAATAGCACAATCAATTTTACCTAAGCACCTGCTTACTTTAGCATTT 60

QY 61 TTAATGTCTTCATTTGCCCTTTGCTATATGGTAGGCAATGCTGTGCTCATCTTAGCTTT 120

Db 61 TTTATGTCTCTAGTAGCTTTTGTCTATTAATGCTAGGAAATGCTTTGCTATTTTAGCTTT 120

QY 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180

Db 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGGCATCTCT 180

QY 181 GACTTCTCTGGTGTGATTTTCCATTCCTGTACATCCCTCACGCTGTTTAACTGG 240

Db 181 GACTTCTTGTGGTGTGATCTCCATTCCTTGTACATCCCTCACGCTGTTTAACTGG 240

QY 241 AATTTTGGAGTGGATCTGCATGTTTTCGCTCATCTACTGCTATCTTTTGTGACGCA 300

Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCCTACTGACTATCTGTTATGTACGCA 300

QY 301 TCTGTCTACAATATTGTCCTCCTTAGCTACGATCGATACGAGTCAAGTTCAGATGCTGTG 360



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Db 301 TCTGTATATAAATGTCCTCATAGCTATGATCGATACCTGTCTCAATGCTGTG 360
Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATGTTGCTCAATGGTGGCTGTTGG 420
Db 361 TCTTATAGAACTCAACATACCTGGGCTCTGAAGATGTTACTCTGATGGTGGCTGTTGG 420
Qy 421 ATACTGGCTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTCCTTGGGAAGAACAGC 480
Db 421 GTGTGGGCTTCTTAGTGAATGGGCAATGATTTCTAGTTTCAGAGTCTTGAAGGA--- 476
Qy 481 ACRAACAAAGGACTGTGAGCTGGCTTGTTCAGAGTGTGATACCTCCTCAGATTACA 540
Db 477 --TGAGTAGTAATGTAAGCTCGATTTTTTTCGGAATGGTACATCCTTGCCATCACA 534
Qy 541 ATGCTCTTGGAAATCCTGCTTCTGTCATCTCTGGGCTTATTTCAATGTACAGATTTTAC 600
Db 535 TCATTCTTGGAAATCGTGATCCAGTCATCTTAGTCGCTTATTTCAACATGATATTTAT 594
Qy 601 TGGAGCCTGTGGAAGCTGAGGCTCTCAGTAGTGCTGCTAGCCATGCTGGATTTCTCCACT 660
Db 595 TGGAGCCTGTGGAAGCTGATCATCTCAGTAGTGCTGCAAGGCAATCCTGGACTGACTGCT 654
Qy 661 ACCCTTCCAGTCTTCAAGACACTTACAGAGCTGGGGTGGCTTGCAGGACAGTAAT 720
Db 655 GTCTCTTCCAAATCTGTGGACACTCATTTCAAGAGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCGTGAATGAAGGATCAGCTCTCTGTCCTCAGTCAAGAAAGTCTTCAAGAAAGAGCAGC 780
Db 715 TCTGATCGACAGAAAGTCTTCTGATCTCTTCAATCAGAGACAGAGAGAGAGTAGT 774
Qy 781 ATCTGTGTCTTAAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAAGTGGGTTCC 840
Db 775 CTATGTTTCTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAATGGTTCC 834
Qy 841 TTCTGGCAATCGGAAGTGCAGCGCTTCGCCAAGGAGTAGCGCAGAGCTTCTCAGAGC 900
Db 835 TTCTCCCAATCAGATTTCTGTAGCTTCTCACCAGGGAACATGTTGAACCTGCTAGAGCC 894
Qy 901 AGGAAGCTAGCAGCTCACTGGCCATCTTCTGAGCGCTTTTGGCCATTTGCTGGGCTCCA 960
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954
Qy 961 TACTGTCTGTTTCAAAATGCTCTTTCATCTTCACTACCCAGAGGAGAGCCCAATCGGTG 1020
Db 955 TATTCTGTGTTCAAAATGCTCTTTCATTTTATTCTCAGCAACAGGTCCTAAATCAGTT 1014
Qy 1021 TGGTACAGATTCCTTCTGCTGCAATGGTTCAATTCGTTTGTATTCCTTCTGTAC 1080
Db 1015 TGGTATAGAAATGCAATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTGTAT 1074
Qy 1081 CCTTTGTCTCAGGCGTTTCCAGAGGCTTTCTGGAAGATACTTTGTGTCAGAAAGCAA 1140
Db 1075 CCATTGTCTCAGAGCGCTTTCAAAGGCTTTCTGGAAGATATTTTGTATAAAGGONA 1134
Qy 1141 CCAGCGCTGTCCAGAAAC---CAGTCAGTATCTTCTTCA 1176
Db 1135 CCTCTACCATCACACACAGTCGGTCACTTCTTCTTAA 1173
```

## RESULT 10

AAI70980

ID AAI70980 standard; cDNA; 1173 BP.

XX

AC AAI70980;

XX

18-MAR-2002 (first entry)

XX

Human histamine H4 receptor cDNA.

XX

KW Histamine H4 receptor; human; antiasthmatic; antiallergenic;

KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;

KW diagnosis; gene therapy; ss.

XX Homo sapiens.

XX WO200192485-A1.

XX 06-DEC-2001.

XX 22-FEB-2001; 2001WO-US005914.

XX 31-MAY-2000; 2000US-0208260P.

XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Lovenberg T, Liu C;

XX WPI; 2002-114339/15.

XX P-PSDB; AAM50564.

New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.

Claim 4; Fig 1; 92pp; English.

The present sequence is that of cDNA clone pH4r encoding a human histamine receptor of the H4 subtype. The cDNA was isolated from a bone marrow cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AA170980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the human histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity

SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match

Best Local Similarity 58.4%; Score 686.6; DB 6; Length 1173;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTACAGTACTGGCATCTTGCCACCAGCTGCTCAGTCCCTTGGCATTT 60

Db 1 ATGCCAGATACTAATAGCACAAATCAATTTATCATAAGCACTCGTGTACTTTAGCATTT 60

Qy 61 TTAATGCTTCATTTGCTTTGCTTATTAATGTTAGGCAATGCTGTGGTCATCTTAGCCCTTT 120

Db 61 TTTATGCTTCATTTGCTTTGCTTATTAATGTTAGGCAATGCTGTGGTCATCTTAGCCCTTT 120

Qy 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180

Db 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180

Qy 181 GACTTCTCTGGGTTTGGATTTCCATTCCTCTGTACATCCCTCAGTGTGTTTAAGTGG 240

Db 181 GACTTCTCTGGGTTTGGATTTCCATTCCTCTGTACATCCCTCAGTGTGTTTAAGTGG 240

Qy 241 AATTTTGGAGTGAATCTGCATGTTTGGCTTATTAATGCTATCTTTTGTGACACCGCA 300

Db 241 GATTTTGGAGGAAATCTGTGTAATTTGGCTACTACTGACTATCTGTTATGTATGACGA 300

Qy 301 TCTGTCTCAATATTTGCTCTCATTAGCTACGATCGATACCAGTCAGTTTCAATGCTGTG 360

Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTGTCAGTCTCAATGCTGTG 360

Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGTTGCTCAATGGTGGCTGTTGG 420

Db 361 TCTTATAGAACTCAACATACTAGGGGCTTTGAAGATTTGTTACTCTGATGGTGGCGGTTGG 420



XX	Human orphan GPCR cDNA, RUP7.	
XX	Human; G protein-coupled receptor; GPCR; research tool; gene; ss.	
XX	Homo sapiens.	
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FH	Key	Location/Qualifiers
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FT		/*tag= a
FT		/product= "Human GPCR protein"
XX		
PN	US2003148450-A1.	
XX		
PD	07-AUG-2003.	
XX		
PF	17-OCT-2002; 2002US-00272983.	
XX		
PR	20-NOV-1998; 98US-0109213P.	
PR	16-FEB-1999; 99US-0120416P.	
PR	26-FEB-1999; 99US-0121852P.	
PR	12-MAR-1999; 99US-0123946P.	
PR	12-MAR-1999; 99US-0123949P.	
PR	28-MAY-1999; 99US-0136436P.	
PR	28-MAY-1999; 99US-0136437P.	
PR	28-MAY-1999; 99US-0136439P.	
PR	28-MAY-1999; 99US-0136567P.	
PR	28-MAY-1999; 99US-0137112P.	
PR	28-MAY-1999; 99US-0137113P.	
PR	29-JUN-1999; 99US-0141448P.	
PR	28-SEP-1999; 99US-0156333P.	
PR	29-SEP-1999; 99US-0156555P.	
PR	29-SEP-1999; 99US-0156634P.	
PR	12-OCT-1999; 99US-00417044.	
XX		
PA	(CHEN/) CHEN R.	
PA	(DANG/) DANG H T.	
PA	(LIAW/) LIAW C W.	
PA	(LINI/) LIN I.	
XX		
PI	Chen R, Dang HT, Liaw CW, Lin I;	
XX		
DR	WPI; 2003-897571/82.	
DR	P-PSDB; ADG98760.	
XX		
PT	New cDNA encoding a human G protein coupled receptor, useful for making a	
PT	probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR	
PT	identification of the expression of the receptor in tissue samples.	
XX		
XX	Claim 25; SEQ ID NO 13; 52pp; English.	
XX		
CC	The present invention provides novel human G protein-coupled receptor	
CC	(GPCR) proteins and their encoding nucleic acids. The invention is useful	
CC	for making a probe for dot-blot analysis and for RT-PCR identification of	
CC	the expression of the receptor in tissue samples. The invention is also	
CC	useful for identifying candidate compounds as inverse agonists, agonists	
CC	or partial agonists and as research tools in determining the location of	
CC	the receptors within the body. The present sequence is human orphan G	
CC	protein-coupled receptor cDNA.	
XX		
SQ	Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;	
	Query Match	58.4%; Score 686.6; DB 10; Length 1173;
	Best Local Similarity	75.1%; Pred. No. 3.4e-204;
	Matches 886; Conservative	0; Mismatches 284; Indels 9; Gaps 2
Qy	1	ATGTGCGAGTCTAACAGTACTGGCATCTTGGCCACGAGCTGCTCAGGTCCCTTGGCATTT 60
Db	1	ATGCCAGATCTAATAGCACAATCAATTTATCATTAGCACTCGTGTACTTTAGCATTT 60
Qy	61	TTAATGCTTTTCATTTGGCTTTGGCTTATTAATGGTAGGCAATGCTGGGTCACTTTAGCCTTT 120
Db	61	TTTATGTCCTTAGTAGCTTTTGGCTATTAATGTTAGGAATGCTTGGTCACTTTAGCTTTT 120

DT 11-M

121 GTGTTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTCT 180  
121 GTGTTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTCT 180  
181 GACTTCTCGTGGGTTGATTTTCCATTCTCTGTAGATCCCTCACGCTGTGTTAACTGG 240  
181 GACTTCTTGTGGGTGATCTCCATTCCTTGTACATCCCTCACGCTGTGTTAACTGG 240  
241 AATTTTGGAAAGTGGATCTGCATGTTTGGCTCATTAATCTGATCTATCTTTGTGCACGGA 300  
241 GATTTTGGAAAGGAAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300  
301 TCTGTCTACAAATATGTCCTCATTTAGCTACGATACGATACGAGTCAGTTCAATGCTGTG 360  
301 TCTGTATATACATTTGCTCTCATCTATGATGATCTGATCTGATCTCAATGCTGTG 360  
361 TCTTATAGGCTCAACACACTGGCATCTGCAAGATTGTTGCTCAAAATGGTGGCTGTTGG 420  
361 TCTTATAGAACTCAACATCTGGGCTTGAAGATTGTTACTCTGATGGTGGCGTTGG 420  
421 ATACTGGCTTCTTGTGAATGCGCGATGATTTCTGCTTCAGATTTCTTGGAAAGACAGC 480  
421 GTGCTGGCTTCTTAGTGAATGGGCAATGATTTCTAGTTTTCAGAGCTTTGGAAAGGA 476  
481 ACGAACACAAAGGACTGTGAGCTGCTTGTGTACAGAGTGGTACATCTCACCATTACA 540  
477 --TGAAGTAGTAATGTGNACTGGATTTTTTTCGGAATGGTACATCTTGCATCACA 534  
541 ATGCTCTTGGAAATTCCTGCTTCTGTCATCTGCTGCTTATTTCAATGTACAGATTTAC 600  
535 TCATTTCTTGGAAATTCGTCATCTGTCAGTCTTATTTCAACATGATATTTAT 594  
601 TGAGGCTGTGGAAGGTAGGGCTCTCAGTAGTGGCTTAGCCATGCTGGAATCTCACT 660  
595 TGGAGCTGTGGAAGGTGATCATCTCAGTAGTGGTCCAAAGCCATCTCTGACTGCT 654  
661 ACCTCTTCAGTCTTCAGGACACTTACACAGAGCTGGGTGGTGGCAGGACAAGTAAT 720  
655 GTCTCTTCCAACTCTGTGGAACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTTT 714  
721 CTTGGATTGAAGGAATCAGCTGATCTCTGTCATCTCAGAAAGTCTCTCGAAGAAAGACAGC 780  
715 TCTGATCGACAGAAGTCTCTGATCTCTTTCATTCAGAGAGACAGAGGAGAGAGTAGT 774  
781 ATCTGTGTCTTAAGGACTACATGAACAGCAGTATCACTGCTTCAAAAGTGGTTC 840  
775 CTATGTTTCTTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAGTGGTTC 834  
841 TCTGCGGATCGAAGGTGAGCGCTTCGCAAGGGAGTACGACAGCTTCTCAGAGC 900  
835 TTTCCCAATCAGATTTCTGTAGCTCTTCCAAAGGGAACATGTTGAAGTCTTAGAGC 894  
901 AGAAGCTAGCCAGGTCACCTGGCCATCTCTCTGAGCGCTTTTGGCAATTTGCTGGGCTCA 960  
895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGGCTCCA 954  
961 TACTGTCTGTTCAAATGTCCTTTCACTTACCAGAACGGAAGCGCCCAATCGGTG 1020  
955 TATTCTCTGTTCAAATGTCCTTTCACTTTATTTCTCAGCAACAGGCTCTTAATCAGTT 1014  
1021 TGGTACAGCATTCCTTCTGGCTGCAATGTTCAATTTCTGTTTCTTAATCTCTTTCTGTAC 1080  
1015 TGGTATAGAAATTCATTTTGGCTCAGTGGTTCATTTCTTTGTCAATCTCTTTTGTAT 1074  
1081 CTTTGTGTACAGGGCTTTCCAAAGGCTTTCTGGAAGTACTTTTGTGACAAAGCAA 1140  
1075 CCATTGTGTACAGGCTTTCCAAAGGCTTTCTGGAAGTACTTTTGTGTAATAAAGCAA 1134  
1141 CAGGCGTGTACAGAAC---CAGTCAGTATCTTCTGA 1176  
1135 CCTCTCCATCACAACACAGTCGGTCAATCTTCTTAA 1173

RESULT 13  
ABS57063  
ID ABS57063 standard; cDNA; 1173 BP.  
XX  
AC ABS57063;  
XX  
DT 28-JAN-2003 (first entry)  
XX  
DE Human cDNA encoding G-protein coupled receptor AXOR35.  
XX  
KW Human; ss; gene; G-protein coupled receptor; AXOR35; lymphocyte;  
KW macrophage; eosinophil; neutrophil; infection; transplant rejection;  
KW gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;  
KW Crohn's disease; irritable bowel syndrome; vomiting; inflammation;  
KW atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;  
KW psoriasis; urological disease; urinary retention; cardiovascular disease;  
KW myocardial infarction; hypertension; cough; renal disease;  
KW chronic obstructive pulmonary disease; atherosclerosis; psychosis;  
KW renal ischaemia; arteriosclerosis; anorexia; anxiety; schizophrenia;  
KW neurological disorder; migraine; anxiety; stroke; septic shock;  
KW dyskinesia; Parkinson's disease; cancer; osteoporosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
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FT /tag= a  
FT /product= "AXOR35"  
XX  
PN US2002137054-A1.  
XX  
PD 26-SEP-2002.  
XX  
PF 20-JUL-2001; 2001US-00910411.  
XX  
PR 02-NOV-1999; 99US-00431898.  
PR 03-FEB-2000; 2000US-00497790.  
PR 20-OCT-2000; 2000US-00693761.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
XX Aubart KM, Bergena DJ, Fitzgerald L, Graybill TL, Li X;  
XX Michalovich D, Morrow DM, Zhu Y;  
XX WPI; 2003-074982/07.  
XX P-PSDB; ABG71960.  
XX  
XX Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for  
XX treating infections, gastrointestinal disorders, autoimmune disorders,  
XX urological diseases, cardiovascular diseases and cancer.  
XX  
XX Claim 2; Page 21-22; 24pp; English.  
XX  
XX The invention relates to an isolated G-protein coupled receptor  
XX polypeptide, AXOR35, (and its homologues and variants) and its encoding  
XX polynucleotide (and its homologues, variants, complements and RNA  
XX equivalents). Also included are an anti-AXOR35 antibody, an AXOR35  
XX expression vector, producing a recombinant host cell by introducing the  
XX vector into a cell such that the host cell produces AXOR35, a membrane of  
XX the host cell expressing AXOR35, identifying/screening for agonists or  
XX antagonists of AXOR35 and inhibiting or promoting the function of  
XX lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,  
XX by administering to the patient AXOR35 agonists or antagonists. The  
XX agonist or antagonist identified is useful for treating a disease such as  
XX asthma, or for inhibiting or promoting the function of lymphocytes,  
XX macrophages, eosinophils, or neutrophils in diseased tissue such as an  
XX asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays,  
XX for identifying compounds that are agonists or antagonists of AXOR35, as  
XX vaccines, or for treating infections (bacterial, fungal, protozoan or  
XX viral infections), transplant rejection, gastrointestinal disorders (such

CC	as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),
CC	irritable bowel syndrome, vomiting, inflammation (such as atopic
CC	dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,
CC	psoriasis), neurological diseases (such as urinary retention),
CC	cardiovascular diseases (such as myocardial infarction), hypotension,
CC	hypertension, pulmonary disorders (such as chronic obstructive pulmonary
CC	disease), cough, renal diseases (such as renal ischaemia),
CC	arteriosclerosis, atherosclerosis, psychotic and neurological disorders
CC	(such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such
CC	as Parkinson's disease), cancer, obesity, stroke, septic shock, graft
CC	versus host disease and osteoporosis. The present sequence is the cDNA
CC	encoding AXOR35
XX	
SQ	Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
	Query Match 58.4%; Score 686.6; DB 10; Length 1173;
	Best Local Similarity 75.1%; Pred. No. 3.4e-204;
	Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
Qy	1 ATGTCGGAGTCTAACAGTACTGGCACTTGGCCACGAGTGTCTCAGGTCCTTGGCATTT 60
Db	1 ATGCAGATAGCAATATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATT 60
Qy	61 TTAATGCTCTCATTTGCTTTGCTATATAGTAGCAATGCTGTGGTCACTTAGCCCTTT 120
Db	61 TTTATGCTCTTAGTAGCTTTTGGCTATATAGTAGGAAATGCTTTGGTCACTTTAGCTTTT 120
Qy	121 GTGTGGACAGAACTTTAGACATCGAAGTAAATTTTCTTAAATTTGGCTATTTCT 180
Db	121 GTGTGGACAAACCTTAGACATCGAAGTAGTAAATTTTCTTAACTTTGGCCATCTCT 180
Qy	181 GACTTCTCGTGGTGTGATTTCCATCTCTGTACATCCCTCAGTGTGTTGTTAACTGG 240
Db	181 GACTTCTTGTGGGTGATCTCCATCTCTTGTACATCCCTCAGCAGCTGTTCGAATGG 240
Qy	241 AATTTTGAAGTGGATCTGATGTTTGGCTCATCTACTGATATCTTTTGTGCACCCCA 300
Db	241 GATTTTGAAGAGGAATCTGTGTATTTTGGCTCACTACTGATATCTGTTATGTACAGA 300
Qy	301 TCTGTCTACAATATTGCTCCTCATTAGCTACGATCGATACCACTCAGTTTCAAAATGCTGTG 360
Db	301 TCTGTATATACATGTCTCATCAGCTATGATCGATACCTGTGATCTCAATGCTGTG 360
Qy	361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATGTTGTCTCAAAATGGTGGCTGTTTGG 420
Db	361 TCTTATAGAACTCAACATACTGGGTCTTGAAGATTGTTACTCTGATGTGGCCGTTTGG 420
Qy	421 ATACTGGCTTTCTGGTAAATGGCCGATGATTTGGCTTCAGATTTCTTGGGAAGAACAGC 480
Db	421 GTGCTGGCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGGNAGGA---- 476
Qy	481 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGTATCCTCACCATTACA 540
Db	477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTATCCTTGGCCATACA 534
Qy	541 ATGCTCTTGGAAATTCCTGCTTCTGTCTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600
Db	535 TCATTCTTGAATTCGTGATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTAT 594
Qy	601 TGGAGCTGTGGAGCGTAGGGCTCTCAGTAGGTGGCCCTAGCCATGCTGGATTTCTCCACT 660
Db	595 TGGAGCTGTGGAGCGTGTATCATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGACTGCT 654
Qy	661 ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGTGGCTTGCAGGACCAAGTAAT 720
Db	655 GTCTCTTCCAACTCTGTGGAACTCATTTACAGAGTAGACTATCTTTCAAGGAGATCTCTT 714
Qy	721 CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCTCGAAGAAAGAGCAGC 780
Db	715 TCTGCATCGACAGAGTTCTCGTGCATCTCTTTCATTACAGAGACAGAGAGAGTAGT 774
Qy	781 ATCTGTGTCTTAAAGACTCACATGAACAGCAGTATCACTGCTTCAAAATGGGTTC 840

Db	775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATGTCTTCCAAAATGGGTCC 834
Qy	841 TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTAGCGCAGAGCTTCTCAGAGGC 900
Db	835 TTCTCCCAATCAGATTTCTGTAGCTTTCACCAAGGGAACATGTTGAACCTGCTTAGAGCC 894
Qy	901 AGGAAGCTAGCCAGGTCTACCTGGCCATCTCTCTGAGCGCTTTTGGCCATTTGCTGGGCTCA 960
Db	895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTTGTGCTGGGCTCA 954
Qy	961 TACTGTCTGTTCACAATTTGCTCTTCACTTACCCAGAACGCGCCCAAAATCGGTG 1020
Db	955 TATTCTCTGTTCACAATTTGCTCTTCACTTATTTCTCAGCAACAGGCTCTAAATCAGTT 1014
Qy	1021 TGGTACAGCATTTGCTCTCTGGCTGCAATGGTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080
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Qy	1081 CCTTTGTGTACAGCGGTTTCCAGAGGCTTTCAGAAAGCTTTCGGAAGATACCTTTGTGACAAAGCAA 1140
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ADJ26922	
ID	ADJ26922 standard; cDNA; 1173 BP.
XX	
AC	ADJ26922;
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	Human endogenous orphan G-protein coupled receptor RUP7 cDNA.
XX	
KW	Human; G protein-coupled receptor; GPCR; dot-blot analysis;
KW	pharmaceutical agent; gene; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	1..1173
FT	/*tag= a
FT	/product= "Human endogenous orphan GPCR protein"
XX	
FN	US2003175891-A1.
XX	
PD	18-SEP-2003.
XX	
PF	21-MAR-2003; 2003US-00393807.
XX	
PR	20-NOV-1998; 98US-0109213P.
PR	16-FEB-1999; 99US-0120416P.
PR	26-FEB-1999; 99US-0121852P.
PR	12-MAR-1999; 99US-0123946P.
PR	12-MAR-1999; 99US-0123949P.
PR	28-MAY-1999; 99US-0136436P.
PR	28-MAY-1999; 99US-0136437P.
PR	28-MAY-1999; 99US-0136439P.
PR	28-MAY-1999; 99US-0136567P.
PR	28-MAY-1999; 99US-0137127P.
PR	28-MAY-1999; 99US-0137131P.
PR	29-JUN-1999; 99US-0141448P.
PR	28-SEP-1999; 99US-0156333P.
PR	29-SEP-1999; 99US-0156555P.
PR	29-SEP-1999; 99US-0156634P.
PR	29-SEP-1999; 99US-0156653P.
PR	01-OCT-1999; 99US-0157280P.
PR	01-OCT-1999; 99US-0157281P.
PR	01-OCT-1999; 99US-0157282P.
PR	01-OCT-1999; 99US-0157293P.





PR 12-MAR-1999; 99US-0123945P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123948P.  
 PR 12-MAR-1999; 99US-0123949P.  
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 PR 28-MAY-1999; 99US-0138438P.  
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 PR 27-AUG-1999; 99US-0151114P.  
 PR 03-SEP-1999; 99US-0152524P.  
 PR 29-SEP-1999; 99US-0156555P.  
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 PR 01-OCT-1999; 99US-0157294P.  
 PR 12-OCT-1999; 99US-00416760.  
 XX (CHEN//) CHEN R.  
 PA (LIAN//) LIAN C W.  
 PA (LOWI//) LOWITZ K.  
 PA (CHAL//) CHALMERS D T.  
 PA (BEHA//) BEHAN D P.  
 XX  
 PI Chen R, Liaw CW, Lowitz K, Chalmers DT, Behan DP;  
 XX  
 DR WPI; 2004-052038/05.  
 DR P-PSDB; ADG86375.  
 XX  
 PT New cDNA encoding a non-endogenous, constitutively activated version of a  
 PT human G protein-coupled receptor, useful for identifying receptor,  
 PT inverse or partial agonists having potential applicability as therapeutic  
 PT agents.  
 XX  
 PS Example 1; SEQ ID NO 13; 110pp; English.  
 XX  
 CC The invention relates to a cDNA encoding a non-endogenous, constitutively  
 CC activated version of a human G protein-coupled receptor comprising hARE-  
 CC 3 (F313K), hARE-4 (V233K), hARE-5 (A240K), hGPCR14 (L257K), hGPCR27 (C283K),  
 CC hARE-1 (E232K), hARE-2 (G285K), hPRP1 (L239K), hG2A (K232A), hRUP3 (L224K),  
 CC hRUP5 (A236K), hRUP6 (N267K), hRUP7 (A302K), hCHN4 (V236K), hMC4 (V244K),  
 CC hCHN3 (S284K), hCHN6 (L352K), hCHN8 (N235K) or hH9 (F236K). Also included are  
 CC a non-endogenous version of a human G protein-coupled receptor encoded by  
 CC the cDNA, a plasmid comprising the vector and the cDNA and a host cell  
 CC comprising the plasmid. The cDNA encodes a non-endogenous, constitutively  
 CC activated version of a human G protein-coupled AT1 receptor comprising  
 CC the angiotensin II type 1 receptor hAT1 (F239K), hAT1 (N114),  
 CC hAT1 (AT2K2551C3, a domain swap mutant) or hAT1 (A243+). The mutation is of  
 CC an amino acid 16 residues from the proline in transmembrane domain 6 and  
 CC is usually to a lysine. The cDNA is useful for identifying candidate  
 CC compounds as receptor agonists, inverse agonists or partial agonists  
 CC having potential applicability as therapeutic agents. The present  
 CC sequence is a cDNA (or fragment) for a wild-type human GPCR.  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 G; 231 C; 403 T; 0 U; 0 Other;  
 Query Match 58.4%; Score 686.6; DB 12; Length 1173;  
 Best Local Similarity 75.1%; Pred. No. 3.4e-204;  
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
 QY 1 ATGTCGAGTCTAACAGTACTGGGATCTTGGCACCAGCTGCTCAGGTCCCTTGCCATT 60  
 DB 1 ATGCCAGATACATAAGACCAATCAATTTATCACTTACCACTCGTGTACTTTAGCATTT 60  
 QY 61 TTAATGCTTCAATTTGCTTATATGAGCAATGCTGTGGTCACTTTAGCCCTTT 120

Db 61 TTTATGCTCTTAGTAGCTTTTGGCTATATAATGCTAGGAATGCTTTGGTCACTTTTAGCTTTT 120  
 QY GTGTGGACAGAAACCTTAGACATCGAAGTAATATATTTTCTTAATTTGGCTATTTCT 180  
 Db GTGTGGACAGAAACCTTAGACATCGAAGTAATATATTTTCTTAATTTGGCTATTTCT 180  
 QY GACTTCTCTGCGGGTTGATTTCCATTTCTCTGTACATCCCTCAGCTGTGTTAACTGG 240  
 Db GACTTCTCTGCGGGTTGATTTCCATTTCTCTGTACATCCCTCAGCTGTGTTAACTGG 240  
 QY AATTTTGGAGTGGAACTGCTGTTTGGGCTCATTTACTGACTATCTTTTGGACCCGA 300  
 Db GATTTTGGAAAGGAAATCTGTATTTTGGGCTCACTACTGACTATCTGTATGTACAGCA 300  
 QY TCTGTCTACAATATTTGCTCTCATTTAGCTACCATCGATCAGTTTCAAAATGCTGTG 360  
 Db TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTGCTCAATGCTGTG 360  
 QY TCTTATAGGGCTCAACACATCGGCTCATGAAGATTTGTCTCAAAATGCTGTGTTGG 420  
 Db TCTTATAGAACTCAACATCTGCGGTCTTGAAGATTTGTACTCTGATGCTGCGCGTTGG 420  
 QY ATACTGCGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTTCTTGGNAGACAGC 480  
 Db GTGCTGCGCTTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCTAGAGTCTTGGAAAGGA 476  
 QY ACGAACACAAAGGACTGTGAGCTGGCTTTGTATACAGAGTGGTACATCCTCACCATTACA 540  
 Db --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGNATGGTATCATCTTGGCCATACA 534  
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 Db GTCTCTTCCAACTCTGTGGACACTTTCAGAGTAGACTATCTTCAGAGAGATCTCTT 714  
 QY CCTGGATGAAGGAATCAGCTGCTCATCTCGTCACTCAGAAAGTCTCTCGAAGAAAGCAGC 780  
 Db TCTGCATCGACAGAAATTTCTGCTCATCTTTCATTTACAGAGACAGAGAGAGAGTAGT 774  
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 Db CTCAATGTTTCTTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGTTTCC 834  
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 Db TTCTCCCAATCAGATTTCTAGCTCTTCCAAAGGGAACATGTTGAATCTCTTAGAGCC 894  
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 QY TGGTACAGCATTTGCTTCTGCTGCAATGTTCAATTTGTTTGTATTCCTTCTCTGTAC 1080  
 Db TGGTATAGAAATGCAATTTTGGCTTCACTGTTCAATTTCTTGTCAATCTCTTTTGTAT 1074  
 QY CTTTGTGTACAGGCGTTTCCAGAGGCTTTCTTGGAAAGATCTTTGTGTGACAAAGCAA 1140  
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 Db CCTCTACCATCACAAACACAGTCGTCAGTATCTTCTTAA 1173

Search completed: April 6, 2005, 23:00:59  
Job time : 737 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 22:36:52 ; Search time 236 Seconds  
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	686.6	58.4	1173	US-09-414-010-1	Sequence 1, Appli
2	686.6	58.4	1173	US-09-812-216-1	Sequence 1, Appli
3	172.8	14.7	1239	US-09-891-053-2	Sequence 2, Appli
4	172.8	14.7	2700	US-09-891-053-5	Sequence 5, Appli
5	143.2	12.2	1338	US-09-165-543-6	Sequence 6, Appli
6	143.2	12.2	1953	US-09-891-053-26	Sequence 26, Appli
7	143.2	12.2	3244	US-09-165-543-4	Sequence 4, Appli
8	140.4	11.9	1335	US-08-985-090-3	Sequence 3, Appli
9	140.4	11.9	1335	US-09-165-543-3	Sequence 3, Appli
10	140.4	11.9	1335	US-09-167-354-6	Sequence 6, Appli
11	140.4	11.9	1335	US-09-642-855-6	Sequence 6, Appli
12	140.4	11.9	1335	US-09-642-514-6	Sequence 6, Appli
13	140.4	11.9	2050	US-09-891-053-21	Sequence 21, Appli
14	140.4	11.9	2665	US-09-949-016-5059	Sequence 5059, Ap
15	140.4	11.9	2689	US-08-985-090-1	Sequence 1, Appli
16	140.4	11.9	2689	US-09-165-543-1	Sequence 1, Appli
17	140.4	11.9	2699	US-09-167-354-5	Sequence 5, Appli
18	140.4	11.9	2699	US-09-642-855-5	Sequence 5, Appli
19	140.4	11.9	2699	US-08-642-514-5	Sequence 5, Appli
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21	94	8.0	1086	US-09-165-543-33	Sequence 33, Appli
22	94	8.0	2218	US-08-985-090-4	Sequence 4, Appli
23	94	8.0	2218	US-09-165-543-31	Sequence 31, Appli
24	93.8	8.0	1056	US-09-524-162-1	Sequence 1, Appli
25	72.6	6.2	1893	US-09-891-053-13	Sequence 13, Appli
26	72.6	6.2	9293	US-09-949-016-16801	Sequence 16801, A
27	72	6.1	601	US-09-949-016-177027	Sequence 177027,

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ALIGNMENTS

RESULT 1

US-09-414-010-1  
; Sequence 1, Application US/09414010  
; Patent No. 6204017  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monsma, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/414,010  
; CURRENT FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-414-010-1

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Matches	886;	Conservative	0;	Mismatches	284;
Indels	9;	Gaps	2;		
Qy	1	ATGTCGGAGTCTACAGTACTGGCATCTTCCACACAGCTGCTCAGGTCCCTTGGCACTTT	60		
Db	1	ATGTCAGATATAATAGCAATCAATATATCATAAGCACTCGTGTACTTTAGCACTT	60		
Qy	61	TTAATGTCTTCATTGGCTTTGCTATATGTTAGGCAATGCTGTGGTCATCTTAGCCCTTT	120		
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Qy	121	GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCCT	180		
Db	121	GTGTGGACAAAAACCTTAGACATCGAAGTAGTATTTTTTTTCTTAACCTTGGCATCTCT	180		
Qy	181	GACTTCTCTGGGTGGTGGTTCATCTCTGTACATCCCTCAGTGTGTTGTTTAACTGG	240		
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Qy	241	AATTTTGAAGTGAATCTGCATCTTTGGCTCAATTAAGTATCTTTTGTGACCGCA	300		
Db	241	GAATTTGGAAGGAATCTGTGATTTTGGCTCACTACTGATCTGTTATGTATACAGCA	300		
Qy	301	TCTGTCTACAAATATGTCCTCAATPAGTAGCATGATCCAGTCAAGTTTCAATGCTGTG	360		

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775 CTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 834
841 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
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RESULT 2

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US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069

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; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-812-216-1

Query Match      58.4%; Score 686.6; DB 4; Length 1173;
Best Local Similarity 75.1%; Pred. No. 6.5e-213;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTGGAGTCTAAACAGTACTGGCATCTTGGCCATGCTGCTGCTGCTGCTGCTGCTGCT 60
DB 1 ATGCCAGATACCTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
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DB 595 TGGAGCTGTGGAAGGCTAGGCTCTCAGTAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 654
QY 661 ACCTCTTCCAGTCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
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DB 715 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774
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Qy 1141 CCAGCGCTGTACAGAAC---CAGTCAGTATCTTCTTGA 1176  
Db 1135 CCTCTACCATCACACACAGTGGTCACTATCTTCTTAA 1173

## RESULT 3

US-09-891-053-2  
; Sequence 2, Application US/09891053  
; Patent No. 6750322  
; GENERAL INFORMATION:  
; APPLICANT: Itadani, Hiraku  
; APPLICANT: Takimura, Tetsuo  
; APPLICANT: Nakamura, Takao  
; APPLICANT: Kobayashi, Masahiko  
; APPLICANT: Tanaka, Ken-ichi  
; APPLICANT: Hidaka, Yusuke  
; APPLICANT: Ohca, Masataka  
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS  
; FILE REFERENCE: 06501-083001  
; CURRENT APPLICATION NUMBER: US/09/891,053  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: PCT/JF99/07280  
; PRIOR FILING DATE: 1999-12-24  
; PRIOR APPLICATION NUMBER: PCT/JF98/05967  
; PRIOR FILING DATE: 1998-12-25  
; PRIOR APPLICATION NUMBER: JP 11/145661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1239  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) ... (1239)  
US-09-891-053-2

Query Match 14.7%; Score 172.8; DB 4; Length 1239;  
Best Local Similarity 49.6%; Pred. No. 2.2e-45;  
Matches 562; Conservative 0; Mismatches 557; Indels 15; Gaps 4;  
Qy 3 GTCGGAGTCTAACAGTACTGGCATCTTGCCACCAAGCTGCTCAGGTGCCCTTGGGATTTT 62  
Db 60 GCGGCTGCAGGGGGGGGGGGTCTCGGCTGCTGGACCGCTGCTCGGCTGGCT 119  
Qy 63 AATGCTTCATTGCTTTGCTATAAAGGTAGGCAAGCTGTGTGTCATCTTAGCCTTTGT 122  
Db 120 CATGGCGTCTCATCGTGGCCACAGTACTGGCAACGCGTGTGTGTCATGCTCGCTTGT 179  
Qy 123 GGTGACAGAAACCTTAGACATCGAGTAATATTTTCTTAATTTGGCTATTTCTGA 182  
Db 180 GCGGATTCGAGCGCTCGCCAGCAACAACTTCTTCTGTCTCAACCTCGCCATCTCCGA 239

## RESULT 4

US-09-891-053-5  
; Sequence 5, Application US/09891053  
; Patent No. 6750322  
; GENERAL INFORMATION:  
; APPLICANT: Itadani, Hiraku  
; APPLICANT: Takimura, Tetsuo

Qy 183 CTTCTCTGGGTTTGAATTTCCATTCCTCTGTATACATCCCTCAGCTGTGTTTAAAC---TG 239  
Db 240 CTTCTCTGGGTTGCTTCTGATCCCATTTGTAGTACCTTATGTGTCGACCGGCGTTG 299  
Qy 240 GAATTTTGGAGTGGATCTGTCATGTTTGGCTCATTACTGACTATCTTTTGTGACCGC 299  
Db 300 GACCTTGGCGGGGCTTCTGCAAGCTGTGGTGGTAGACTACCTACTGTGTGCTC 359  
Qy 300 ATCTGTCTACAAATATTTGCTCATTAGCTACGATGATACCACTCAGTTCAGATGCTGT 359  
Db 360 CTCGGTCTTCAACATCTGACTCATCAGCTATGACCGATTTCTGTGCTGACTCTGAGCTGT 419  
Qy 360 GTCTTATAGGCTCAACACACTGTCATCATGAAGATTTGCTCAAAATGGTGGCTTTG 419  
Db 420 CTCCTACAGGCGCCAGCAGGGGGAACAGAGACGGCGCTTCGGAAGATGGCACTGGTGTG 479  
Qy 420 GATCTGGCTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAG-----TTCTTGA 473  
Db 480 GGTCTGGCTTCTGCTGTATGGGCTGCTCCTGAGTTGGGAGTACCTGTCTGGTGG 539  
Qy 474 GAACAGCAGCAACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTATACATCTCAC 533  
Db 540 CAGTTCCATCCCCAGGGGCACTGCTATGCTGAGTTCTTCTACAACTGGTACTTCTCAT 599  
Qy 534 CATTACAATGCTCTTGGAAATTCCTGCTTCTGCTCATCTCTGTGGCTTATTTCAATGTACA 593  
Db 600 CACGGCTTCCACCTCGAGTTCTTTCAGCCCTTCTCAGCGTTAGCTTCTTCAACCTCAG 659  
Qy 594 GATTTACTGGAGCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCTCAGTACCTGCTGATTT 653  
Db 660 CATCTACCTGAACATCCAGAGGCGCACCGCTTTCGGCTTGTATGGGGCGCTGAGGCTGG 719  
Qy 654 CTCCACTACCTTCTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGAC 713  
Db 720 CCAGAACCCCAACAGATGCCAGCCCTGCCACTTCCAGCTCCCCCAGCTGCTGGGG 779  
Qy 714 AAGTAATCTGGAATGAAGGAATCAGCTGCACTCTGCTCACTCAGAAAAGTCTTCGAAGAAA 773  
Db 780 CTGCTGGCCAAAAGGCAATGCGAGGCAATGCCGTTGCACAGCTCTGSCAGCTCTCTCAAG 839  
Qy 774 GAGCAGCATCTGTGTCTTAAAGACTCAATGAAACAGAGTATCATCTGCTTCAAAGT 833  
Db 840 GGGCACTGAGAGGCGCACGCTCACTCA---AAAGGGGCTTCCAAGCCATCAGCATCTTCAGC 896  
Qy 834 GGGTCTCTTCTGCGCATCGGAAGTGCAGCGCTTTCGCCAAAGGGAGTACGACAGCTTCT 893  
Db 897 ATCCCTGGAGAGCGCATGAAGTGGTGTCCAGAGCATCACCCAGCGCTTCCGGCTGTC 956  
Qy 894 CAGAGGCAAGAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGGCATTTGCTG 953  
Db 957 GCGGCAACAAGAGGTGGCCAAAGTCCGTGGCCATCATCTGTAGCATCTTTGGGCTCTGCTG 1016  
Qy 954 GGCTCCATCTGTCTGTTCACAAATGTCTTTTAACTTACCCAGAGCGGAAACGCCCAA 1013  
Db 1017 GCGCGCTGACACGCTCCTTAATGATCATCCGAGCTGCTTGGCATGGCGCTGCATCCCGA 1076  
Qy 1014 ATCGGTGTGTACAGCATTCCTTCTGCTGCAATGTTCAATTCGTTGTTAATCCCTT 1073  
Db 1077 TT---ACTGTGACAGAGCTGCTTCTGGCTTCTGTGGGCAACTCGGCGCTCAACCCGT 1133  
Qy 1074 TCTGTACCTTGTGTGTCACAGCGCTTTCCAGAGGCTTTCTGGAAGTACTTTG 1127  
Db 1134 CCTTACCCACTGTGCCACTACAGTTTCCGAGAGCTTCCACCAAGCTCTCTCTG 1187

```

: APPLICANT: Nakamura, Takao
: APPLICANT: Kobayashi, Masahiko
: APPLICANT: Tanaka, Ken-ichi
: APPLICANT: Hidaka, Yusuke
: APPLICANT: Ohta, Masataka
: TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
: TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
: FILE REFERENCE: 06501-083001
: CURRENT APPLICATION NUMBER: US/09/891,053
: PRIORITY FILING DATE: 2001-09-17
: PRIOR APPLICATION NUMBER: PCT/JP99/07280
: PRIOR FILING DATE: 1999-12-24
: PRIOR APPLICATION NUMBER: PCT/JP98/05967
: PRIOR FILING DATE: 1998-12-25
: PRIOR APPLICATION NUMBER: JP 11/145661
: PRIOR FILING DATE: 1999-05-25
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 2700
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (351)...(1589)
: NAME/KEY: misc feature
: LOCATION: (1)...(2700)
: OTHER INFORMATION: n = A,T,C or G
: US-09-891-053-5

Query Match          14.7%; Score 172.8; DB 4; Length 2700;
Best Local Similarity 49.6%; Pred. No. 3.6e-45;
Matches 562; Conservative 0; Mismatches 557; Indels 15; Gaps 4;

Qy 3 GTCGGAGCTTAA CAGTACTGGCATCTTGGCCACACAGCTGCTCAGTGCCTCCCTTGGCAATTTT 62
Db 410 GCGCGTGCACGGCGGGGCGCGCTCTTCGGCTGCGCTGGACCGCTGCTCTGGCTGGCGCT 469

Qy 63 AATGCTCTTCA TTTGCCCTTGTCTATAAAGTAGGCAATGCTGTGCTCATCTTTAGGCTTTGT 122
Db 470 CATGGCGCTGCTCATCTGTGGCCACAGTACTGGGCAACGCGTGTGCTCATGCTCGCTTCGT 529

Qy 123 GGTGGACAGAAACCTTACATCATCGAAGTAATATTTTTTTCTTAATTTGGCTATTTCTGA 182
Db 530 GCGGGAATTCAGACCTCCGCAACCACTTCTTCTGCTCAACCTCGCCATCTCGA 589

Qy 183 CTTCCTCGTGGTGTGAATTTCCATTCCTCTGTATCATCCCTCACGTGTGTTTAAAC---TG 239
Db 590 CTTCCTCGTGGTGCCTTCTGCATCCCATTTGTACGTACCCCTATGTGCTGACCGGCCGTG 649

Qy 240 GAATTTTGGAGTGAATCTGCATGTTTTGGCTCATTTACTGACTATCTTTTGTGCACGCG 299
Db 650 GACCTTCGGCGGGGCGCTCTGCAAGCTGTGGCTGGTAGACTACCTACTGTGTGCTC 709

Qy 300 ATCTGTCTCAATAATTTGCTCATTAGCTACGATCGATACAGTCAAGTTCAAATGCTGT 359
Db 710 CTGGTCTTTCAAATCGTACTCATCAGCTATGACCGAATCTGTGCTCACTCGAGCTGT 769

Qy 360 GTCATTAGGGCTCAACACACTGGCATCATGAAGATTTGTGCTCAAAATGGTGGCTGTTTG 419
Db 770 CTCCTACAGGGGCCAGCAGGGGGGACACGAGACGGGCGCTTCGGAAGATGGCACTGGTGTG 829

Qy 420 GATACTGGCTTTCTTGTGTAATGGCCCGATGATTTCTGGCTTCAGA-----TTCTTGGAA 473
Db 830 GGTGCTGGCTTCTCTGTGTATGGGCGTGCATCCTGAGTTGGAGTACCTGTCTGTGG 889

Qy 474 GAACAGCACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCCTCAC 533
Db 890 CAGTTCCATCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACAACTGTTACTTCTCAT 949

Qy 534 CATTTACAAATGCTCTTGGAAATTCCTGCTTCCTGTGCATCTCTGTGGCTTATTTCAATGACA 593
Db 950 CAGGGCTCCACCCCTCGAGTTCTTCAGGCCCTTCTCAGGCCCTTCTCAGGCTTACTTCTTCACTCAG 1009

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1338 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
US-09-165-543-6

Query Match 12.2%; Score 143.2; DB 3; Length 1338;
Best Local Similarity 54.2%; Pred. No. 1e-35;
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

Qy 3 GTCGGAGTCTAACAGTACTGGCATCTTCCACCAGCTGCTCAGGTCCCTTGGCAATTTT 62
Db 60 GCGCGCTCAGCGGGGGCGGGCTTCTCGGTCCCTGGACCGCTGCTCTGGTGGCGCT 119

Qy 63 AATGCTTTTCATTTGCTTTGCTATTAAGTATAGGCAAGCTGTGGTCACTTTAGCTTTGT 122
Db 120 CATGCGCTGCTCATCTGGTGGCCACAGTACTGGCAACGCGTGTGCTATGCTCGCTTCGT 179

Qy 123 GGTGGACAGAACCTTAGACATCGNAGTAATATTTTCTTAATTTGGCTATTTCTGA 182
Db 180 GCGGATTCGAGCCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGA 239

Qy 183 CTTCTCTGCTGGTGTGATTTTCATTCCTCTGTACATCCCTCAGGTGTTGTTTAAAC---TG 239
Db 240 CTTCTCTGCTGGTGTGCTTCTGATCCCATTTGATGCTACCTATGCTGACGGCGCTTG 299

Qy 240 GAATTTTGGAAAGTGGAAATCTGCATGTTTGGCTCAATTAAGTCACTATCTTTTGTGACCGC 299
Db 300 GACCTTCGGCGGGGCTCTGCAAGCTGTGGTGTGAGTACTACTGCTGTCGCTC 359

Qy 300 ATCTGTCTCAATATTCCTCATTTAGTATGATGATGATGATGATGATGATGATGATGATGAT 359
Db 360 CTCGGTCTTCAACATCGTACTCATCAGCTATGACCGATTCTCTGTCAGTCACTCGAGCTGT 419

Qy 360 GTCTTTATAGGCTCAACACACTGGCATCATGAAGATTCCTGCTCAATGGTGGCTGTTTG 419
Db 420 CTCCTACAGGGCCCGAGGGGGACACGAGAGGGGCGCTTCGGAAGATGGCACTGGTGTG 479

Qy 420 GATATGCTTTCTTTGGTAAATGGCCCGCATGATTTCTGCTTTCAGA-----TTCTTGGAA 473
Db 480 GGTGCTGCTTCTGCTGTATGAGGCTGCTCCATCTGAGTTGGAGTACCTGCTGTGG 539

Qy 474 GAACAGACAGAACACAAAGGACTGTGACCGCTTGGCTTGTATGAGAGTGGTATCATCTTCAAC 533
Db 540 CAGTTTCCATCCCGAGGGCCACTGCTATGCTGAGTCTTCTTACAACTGGTACTTTCTCAT 599

Qy 534 CATTACAATGCTTTGGAAATTCCTGCTTCTGCTCATCTCTGCTGCTTATTTCAATGTACA 593
Db 600 CACGGCTTCCACCTCGAGTTCTTCACGCGCTTCTCAGCGCTTACCTTCTTCAACCTCAG 659

Qy 594 GATTTACTGGAGCTGTGGAAAGCTGA 619
Db 660 CATCTACCTGAACATCCAGAGGCGCA 685
```

RESULT 6  
US-09-891-053-26  
; Sequence 26, Application US/09891053  
; Patent No. 6750322  
; GENERAL INFORMATION:  
; APPLICANT: Itadani, Hiraku  
; APPLICANT: Takimura, Tetsuo  
; APPLICANT: Nakamura, Takao  
; APPLICANT: Kobayashi, Masahiko  
; APPLICANT: Tanaka, Ken-ichi  
; APPLICANT: Hidaka, Yusuke  
; APPLICANT: Ohta, Masataka  
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)

```

; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891.053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1953
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (302)...(1636)
US-09-891-053-26

Query Match 12.2%; Score 143.2; DB 4; Length 1953;
Best Local Similarity 54.2%; Pred. No. 1.3e-35;
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

Qy 3 GTCGGAGTCTAACAGTACTGGCATCTTCCACCAGCTGCTCAGGTCCCTTGGCAATTTT 62
Db 361 GCGCGCTCAGCGGGGGCGGGCTTCTCGGTCCCTGGACCGCTGCTCTGGTGGCGCT 420

Qy 63 AATGCTTTTCATTTGCTTTGCTATTAAGTATAGGCAAGCTGTGGTCACTTTAGCTTTGT 122
Db 421 CATGCGCTGCTCATCTGTCGCCACAGTACTGGGCAACGCGCTGCTATGCTCGCGCTT 480

Qy 123 GGTGGACAGAACCTTAGACATCGAAGTAAATTTTCTTAATTTGGCTATTTCTGA 182
Db 481 GCGGATTCGAGCTCTCGCACCCAGAACAACTTCTTCTGCTCAACCTCGGCATCTCGA 540

Qy 183 CTTCTCTGCTGGTGTGATTTTCCATTCCTCTGTATACATCCCTCAGCTGTTGTTTAAAC---TG 239
Db 541 CTTCTCTGCTGGTGTGCTTCTGATCCCATTTGTACGTACCTATGCTGTGACGGCGCTTG 600

Qy 240 GAATTTTGGAAAGTGGAAATCTGCAATGTTTGGCTCAATTAAGTCACTATCTTTTGTGACCGC 299
Db 601 GACCTTCGGCGGGGCTCTGCAAGCTGTGGTGTGAGTACTACTGCTGTCGCTC 660

Qy 300 ATCTGTCTCAATATTCCTCATTTAGTATGATGATGATGATGATGATGATGATGATGATGAT 359
Db 661 CTCGGTCTTCAACATCGTACTCATCAGCTATGACCGATTCTCTGTCAGTCACTCGAGCTGT 720

Qy 360 GTCTTTATAGGCTCAACACACTGGCATCATGAAGATTTGTTGCTCAAAATGGTGGCTGTTTG 419
Db 721 CTCCTACAGGGCCCGAGGGGGACACGAGAGGGGCGCTTCGGAAGATGGCACTGGTGTG 780

Qy 420 GATATGCTTTCTTTGGTAAATGGCCCGCATGATTTCTGCTTTCAGA-----TTCTTGGAA 473
Db 781 GGTGCTGCTTCTGCTGTATGAGGCTTGCATCTCTGTCAGTCACTCGAGCTGT 840

Qy 474 GAACAGACAGAACACAAAGGACTGTGAGCGCTTGGCTTGTATACAGAGTGGTATCATCTTCAAC 533
Db 841 CAGTTTCCATCCCGAGGGCCACTGCTATGCTGAGTCTTCTTACAACTGGTACTTTCTCAT 900

Qy 534 CATTACAATGCTTTGGAAATTCCTGCTTCTGCTCATCTCTGCTGCTTATTTCAATGTACA 593
Db 901 CACGGCTTCCACCTCGAGTTCTTCACGCGCTTCTCAGCGCTTACCTTCTTCAACCTCAG 960

Qy 594 GATTTACTGGAGCTGTGGAAAGCTGA 619
Db 961 CATCTACCTGAACATCCAGAGGCGCA 986
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RESULT 7  
US-09-165-543-4  
; Sequence 4, Application US/09165543

Patent No. 6093545  
GENERAL INFORMATION:  
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann  
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/165,543  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,780  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth A. Hanley  
REGISTRATION NUMBER: 33,505  
REFERENCE/DOCKET NUMBER: MNI-032CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 778..2112  
US-09-165-543-4

Query Match 12.2%; Score 143.2; DB 3; Length 3244;  
Best Local Similarity 54.2%; Pred. No. 1.8e-35;  
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

QY 3 GTCGGAGTCTAAACAGTACTGGCATCTTGGCCACGAGCTGCTCAGGTCCCTTGGCATTTTT 62  
DB 837 GCGGGCTGCAGGGGGGGGGGGCTTCTGGCTGCTGGACCGCTGCTGGCTGGCT 896

QY 63 AATGCTTCAATTTGGCTTTGCTAATAAGTGGTAGCAAGTGTGGTCACTTTAGCCTTTGT 122  
DB 897 CATGGCGTCTCATCGTGCCACAGTACTGGGCAACGGCGTGGTCACTGCTGGCTTCT 956

QY 123 GGTGGACAGAACTTAGACATCAAGTAATATTTTCTTAATTTGGCTATTCTGA 182  
DB 957 GCGGAGTTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTGGCCATCTCCA 1016

QY 183 CTTCTCTGGGGTTTGATTTCCATTCTCTGTACATCCCTCAGTGTGTTTAAAC---TG 239  
DB 1017 CTTCTCTGGGGTTCCTTCTGCACTCCATTTAGTACCTATGCTGACCGCGGTG 1076

QY 240 GAATTTTGAAGTGGAACTGCAATTTGGCTCATATCTGACTATCTTTTGGACCGC 299  
DB 1077 GACCTTTGGCGGGGGCTCTGCAAGCTGTGGTGGTAGACTACTACTGTGCTCTC 1136

QY 300 ATCTGTCAAAATATTTGCTCTATTAGCTACGATCGATACCACTCAGTTCCTGCT 359  
DB 1137 CTGGGTCTCAATCTGATCTCATAGCTATGACCAATTCCTGCTCAGTCACTGAGCTGT 1196

QY 360 GTCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTTTTG 419  
DB 1137 CTGGGTCTCAATCTGATCTCATAGCTATGACCAATTCCTGCTCAGTCACTGAGCTGT 1196

QY 63 AATGCTTCTCAATTTGGCTTTGCTAATAAGTGGTAGCAAGTGTGGTCACTTTAGCCTTTGT 122

1197 CTCTACAGGGCCAGAGGGGGACACAGACGGGCGCTTCGGAAGATGGCACTGGTGTG 1256  
QY 420 GATACCTGGCTTCTTGGTAATGGCCGCGATGATCTGGCTTCTGAGTCTTCTGGAA 473  
DB 1257 GGTGCTGGCTTCTTGGTATGATGGGCTTCCCATCTGAGTGGGAGTACTGCTGCTGGTGG 1316  
QY 474 GAACAGCACGAACACAAAGGACTGTGAGCTTGTGAGCTTGTGTACAGAGTGGTATCATCTCAC 533  
DB 1317 CAGTTCCATCCCGAGGGCCACTGCTATGCTGAGTCTTCTACAACTGGTACTTCTCAT 1376  
QY 534 CATTACATGCTCTTGGAAATCT 593  
DB 1377 CACGGCTCCACCTCGAGTCTTCTCAGGCTTCTCTCAGGCTTCTCTCAGGCTTCTCTCAACCTCAG 1436  
QY 594 GATTTACTGGAGCTGTGGAAGGTA 619  
DB 1437 CATCTACCTGAAACATCCAGAGGCGCA 1462

RESULT 8  
US-08-985-090-3  
Sequence 3, Application US/08985090  
Patent No. 5885893  
GENERAL INFORMATION:  
APPLICANT: Andrew D.J. Goodearl  
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,090  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jean M. Silveri  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: MNI-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1335 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1335  
US-08-985-090-3

Query Match 11.9%; Score 140.4; DB 2; Length 1335;  
Best Local Similarity 53.6%; Pred. No. 8.4e-35;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

QY 3 GTCGGAGTCTAACAGTACTGGCATCTTGGCCACGAGTGTCTCAGGTCCCTTGGCATTTTT 62  
DB 60 GCGCGGGGGGGGGGGGGGGGGCTTCTCGGCAAGCTGGACCGGGTGTGGCGCGCT 119  
QY 63 AATGCTTCTCAATTTGGCTTTGCTAATAAGTGGTAGCAAGTGTGGTCACTTTAGCCTTTGT 122

Db 120 CATGGCGTGCATCGTGGCCACCGTGTCTGGGCAACGCGTGGTCAATGCTCGCTCGT 179  
Qy 123 GGTGACAGAACTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTGA 182  
Db 180 GGCCGACTCGAGCTCCGACCCAGACAACTTCTCTGCTCAACCTCGCATCTCGA 239  
Qy 183 CTTCTCGTGGTGGTTGATTTTCATTCCTCTGACATCCCTCAAGTGTG-----TTTAACTG 239  
Db 240 CTTCTCGTGGCGCTTCTGATCCCACTGTATGCTACCTACGCTGACAGGCGCTG 299  
Qy 240 GAAATTTGGAGTGAATCTGATCTTTGGCTCAATTAATGACTATCTTTTGTGACCGC 299  
Db 300 GACCTTCGGCGGGGCGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGTGTGACCTC 359  
Qy 300 ATCTGCTACAAATATTTGCTCATTAGCTACGATACGATACAGTCAAGTTCATAATGCTGT 359  
Db 360 CTCTGCTTCAACATCTGCTCATGACTACGATACGACCGCTCTCTGCTGCTACCGGCGGT 419  
Qy 360 GTCTATAGGCTCAACACATCGCATCATGAAGATTGTGCTCAAAATGGTGGCTGTTG 419  
Db 420 CTCATACCGGGCCAGCAGGGGTGACACGCGGCGGAGTGGGGAAGATGCTGTGTGTG 479  
Qy 420 GATACTGCTTCTGTTAAATGGCCGATGATTTCTGCTTCAAGT-----TCTTGAA 473  
Db 480 GGTGCTGGCTTCTGCTGTACGGACAGCCATCTGAGCTGGGAGTACCTGTCTCGGGG 539  
Qy 474 GAACAGCAGAACACAAAGGAGTGTGAGCTGGCTTGTGTACAGAGTGTATCTCTAC 533  
Db 540 CAGCTCCATCCCGAGGGCAGTGTATGCGAGTTCCTTCAACACTGGTACTTCTCAT 599  
Qy 534 CATTACAATGCTTTGGAATTCCTGCTCATCTCTGCTGCTTATTTCAATGTACA 593  
Db 600 CACGCTTCCACCTGGAGTCTTCTTACGCTTCTCTCAGCGTCACTTCTTTAACTCAG 659  
Qy 594 GATTACTGGAGCTGTGGAAGCTGAGGCTCTCAG 629  
Db 660 CATCTACCTGAACATCCAGAGCGGCACCCGCTCCG 695

RESULT 9

US-09-165-543-3  
; Sequence 3, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D. J. Goodearl and Sandra Gluckman  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MM1-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400

; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1335 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1335  
US-09-165-543-3

Query Match 11.9%; Score 140.4; DB 3; Length 1335;  
Best Local Similarity 53.6%; Pred. No. 8.4e-35;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;  
Qy 3 GTCGGAGTCTAACAGTACTGGCATCTTCCACACAGCTGCTCAGGTCCCTTGGCAATTTT 62  
Db 60 GCGCGCGCGGGCGCGCGCTTCTCGCAGCCTGGACCGCGGTGCTGGCGCGCT 119  
Qy 63 AATGCTTTCATTTTGGCTTGTCTATAATGTTAGGCAATGCTGTGTGCTATCTTTAGCTTTGT 122  
Db 120 CATGGCGTGTCTCATCTGTGCGCCAGCGTCTGGGCAACGCGTGTGCTGCTGCTGCTTCTGT 179  
Qy 123 GGTGACAGAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTGA 182  
Db 180 GGCGAGCTCGAGCTTCGCGACCCAGACAACTTCTTCTGCTCAACCTCGCATCTCGA 239  
Qy 183 CTTCTCGTGGTGGTGGATTTCCATTCCTCTGTATCATCCCTCACGCTGTG-----TTTAACTG 239  
Db 240 CTTCTCGTGGCGCTTCTGCTATCCCACTGTATGTATACCTTACGCTGCTGACAGCGCGCTG 299  
Qy 240 GAAATTTGGAGTGAATCTGCAATGTTTGGCTCATTAATGACTATCTTTTGTGACCGC 299  
Db 300 GACCTTCGGCGGGCGCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGTGTGACCTC 359  
Qy 300 ATCTGCTACAAATATTTGCTCCTCATTAGCTACGATCGATACAGTCAAGTTCATAATGCTGT 359  
Db 360 CTCTGCTTCAACATCTGCTCATCAGTACGACCGCTTCTCTGCTGCTACCCGAGCGGT 419  
Qy 360 GTCTATAGGCTCAACACACTGSCATCATGAAGATTGTGCTCAAAATGGTGGCTGTTG 419  
Db 420 CTCATACCGGGCCAGCAGGGGTGACACGCGCGGCGAGTGGGGAAGATGCTGTGTGTG 479  
Qy 420 GATACTGCTTCTTGGTAATGSCCGGATGATTTCTGCTTCAGAT-----TCTTGAA 473  
Db 480 GGTGCTGGCTTCTGCTGTACGAGCAGCGCATCTCTGAGTGGAGTACCTGTCCGGGG 539  
Qy 474 GAACAGCAGAACACAAAGGAGTGTGAGCTGGCTTGTGTACAGAGTGGTATCTCTCAC 533  
Db 540 CAGCTCCATCCCGAGGGCAGTGTATGCGAGTTCCTTCAACACTGGTACTTCTCAT 599  
Qy 534 CATTACAATGCTTTGGAATTCCTGCTCATCTCTGCTGCTTATTTCAATGTACA 593  
Db 600 CACGCTTCCACCTGGAGTCTTCTTACGCTTCTCTCAGCGTCACTTCTTTAACTCAG 659  
Qy 594 GATTACTGGAGCTGTGGAAGCTGAGGCTCTCAG 629  
Db 660 CATCTACCTGAACATCCAGAGCGGCACCCGCTCCG 695

RESULT 10

US-09-167-354-6  
; Sequence 6, Application US/09167354A  
; Patent No. 6136559  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; TITLE OF INVENTION: SUBTYPE



FILE REFERENCE: JMW  
CURRENT APPLICATION NUMBER: US/09/167,354A  
CURRENT FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 1335  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:CDNA  
US-09-167-354-6

Query Match 11.9%; Score 140.4; DB 3; Length 1335;  
Best Local Similarity 53.6%; Pred. No. 8.4e-35;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;  
QY 3 GTCGAGTCTAAACAGTACTGGCATCTTGGCACCAGCTGCTCAGGTCCCTTGGCATTTT 62  
Db 60 GCGCGCGCGCGCGCGCGCGCTTCTCGGACGCTGGACCGCGGTGCTGGCGCGCT 119  
QY 63 AATGCTTTCATTGGCTTGTCTATAATGTAGGCAATGCTGTGGTCACTTTAGCCCTTGT 122  
Db 120 CATGGCGCTGCTCATCGTGGCCACGCTGCTGGCAACGCGTGTGTCATGCTCGCTTGT 179  
QY 123 GGTGGACAGAACTTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGA 182  
Db 180 GCGCGACTCGAGCTCCGACCCAGAACAACTTCTCTGCTCAACCTCGCATCTCCGA 239  
QY 183 CTTCTCTGGGGTTGATTTCATCTCTGTACATCCCTCAGCTGTG---TTTAACTG 239  
Db 240 CTTCTCTGGCGCTTCTGATCCACTGTATGTATGATGATGATGATGATGATGATGATG 299  
QY 240 GAATTTGGAAGTGAATCTGCAATGCTTTTGGCTCATTTACTGACTATCTTTTGTGCA 299  
Db 300 GACCTTCGCGCGCGCGCTCTGCAAGCTGTGGCTGTGGTGTGGTGTGGTGTGGTGTGG 359  
QY 300 ATCTGTCTACAATATTTGCTCAITTAGTACGATCGATCGATCGATCGATCGATCGAT 359  
Db 360 CTTCTGCTTCAACATCGTGTCTCATCAGCTACGCGCTTCTCTGCGGTCAACCGAGCG 419  
QY 360 GTCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTGTCTCAATGTTGCTTTG 419  
Db 420 CTCATACCGCGCGCGCGCTGACCGCGCGCGCGCTGCGGAGATGCTGTGTGTGTG 479  
QY 420 GATCTGCTTTCTTTGGTAAATGGCCCGATGATTTCTGGCTTCAGAT-----TCTT 473  
Db 480 GGTGCTGGCTTCTGCTGTACGACCGCATCTGAGCTGGGAGTACCTGTCCGGGG 539  
QY 474 GAACAGCAGAACACAAAGGACTGTGAGCTGGCTTTGTACAGAGTGTGATCTCTCAC 533  
Db 540 CAGCTCCATCCCGAGGCGCGCTGCTATGCGGCTTCTTCTACAACTGGTACTTCTCAT 599  
QY 534 CATTACAATGCTCTTGAATTCCTGCTCTCTGCTCATCTCTGCTGGCTTATTTCAATG 593  
Db 600 CACGGCTTCCACCTGGAGTTCTTTACGCGCTTCTTCTACAACTGGTACTTCTCAT 659  
QY 594 GATTACTGAGCTGTGGAAGCGTGTAGGCTCTCAG 629  
Db 660 CATCTACCTGAACATCCAGAGGCGCGCGCGCTCCG 695

RESULT 11  
US-09-642-855-6  
Sequence 6, Application US/09642855  
Patent No. 6413743  
GENERAL INFORMATION:  
APPLICANT: Lovenberg, Timothy  
APPLICANT: Erlander, Mark  
APPLICANT: Pyati, Jayashree  
APPLICANT: Huvar, Arne  
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
SUBTYPE

FILE REFERENCE: JMW  
CURRENT APPLICATION NUMBER: US/09/642,855  
CURRENT FILING DATE: 2000-08-21  
PRIOR APPLICATION NUMBER: 09/167,354  
PRIOR FILING DATE: 1998-10-06  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 1335  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:CDNA  
US-09-642-855-6

Query Match 11.9%; Score 140.4; DB 3; Length 1335;  
Best Local Similarity 53.6%; Pred. No. 8.4e-35;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;  
QY 3 GTCGAGTCTAAACAGTACTGGCATCTTGGCACCAGCTGCTCAGGTCCCTTGGCATTTT 62  
Db 60 GCGCGCGCGCGCGCGCGCGCTTCTCGGACGCTGGACCGCGGTGCTGGCGCGCT 119  
QY 63 AATGCTTTCATTGGCTTGTCTATAATGTAGGCAATGCTGTGGTCACTTTAGCCCTTGT 122  
Db 120 CATGGCGCTGCTCATCGTGGCCACGCTGCTGGCAACGCGTGTGTCATGCTCGCTTGT 179  
QY 123 GGTGGACAGAACTTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGA 182  
Db 180 GCGCGACTCGAGCTCCGACCCAGAACAACTTCTCTGCTCAACCTCGCATCTCCGA 239  
QY 183 CTTCTCTGGGGTTGATTTCATCTCTGTACATCCCTCAGCTGTG---TTTAACTG 239  
Db 240 CTTCTCTGGCGCTTCTGATCCACTGTATGTATGATGATGATGATGATGATGATGATG 299  
QY 240 GAATTTGGAAGTGAATCTGCAATGCTTTTGGCTCATTTACTGACTATCTTTTGTGCA 299  
Db 300 GACCTTCGCGCGCGCGCTCTGCAAGCTGTGGCTGTGGTGTGGTGTGGTGTGGTGTGG 359  
QY 300 ATCTGTCTACAATATTTGCTCAITTAGTACGATCGATCGATCGATCGATCGATCGAT 359  
Db 360 CTTCTGCTTCAACATCGTGTCTCATCAGCTACGCGCTTCTCTGCGGTCAACCGAGCG 419  
QY 360 GTCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTGTCTCAATGTTGCTTTG 419  
Db 420 CTCATACCGCGCGCGCGCTGACCGCGCGCGCGCTGCGGAGATGCTGTGTGTGTG 479  
QY 420 GATCTGCTTTCTTTGGTAAATGGCCCGATGATTTCTGGCTTCAGAT-----TCTT 473  
Db 480 GGTGCTGGCTTCTGCTGTACGACCGCATCTGAGCTGGGAGTACCTGTCCGGGG 539  
QY 474 GAACAGCAGAACACAAAGGACTGTGAGCTGGCTTTGTACAGAGTGTGATCTCTCAC 533  
Db 540 CAGCTCCATCCCGAGGCGCGCTGCTATGCGGCTTCTTCTACAACTGGTACTTCTCAT 599  
QY 534 CATTACAATGCTCTTGAATTCCTGCTCTCTGCTCATCTCTGCTGGCTTATTTCAATG 593  
Db 600 CACGGCTTCCACCTGGAGTTCTTTACGCGCTTCTTCTACAACTGGTACTTCTCAT 659  
QY 594 GATTACTGAGCTGTGGAAGCGTGTAGGCTCTCAG 629  
Db 660 CATCTACCTGAACATCCAGAGGCGCGCGCGCTCCG 695

RESULT 12  
US-09-642-514-6  
Sequence 6, Application US/09642514  
Patent No. 6437100  
GENERAL INFORMATION:  
APPLICANT: Lovenberg, Timothy  
APPLICANT: Erlander, Mark  
APPLICANT: Pyati, Jayashree  
APPLICANT: Huvar, Arne

```

; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE OF INVENTION: SUBTYPE
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-514-6

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Query Match      11.9%; Score 140.4; DB 3; Length 1335;
Best Local Similarity 53.6%; Pred. No. 8.4e-35;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

Qy 3 GTCGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCCTTGGCATTTT 62
Db 60 GCGCGCGCGCGCGCGCGGCTTCTCGGACCTGGACCGGCTGCTGGCGCGCT 119

Qy 63 AATGTCCTTTCATTTGCTTTGCTATATAGTAGGCAATGCTGTGTCATCTTAGCCTTTGT 122
Db 120 CATGGCGCTGCTCATCGTGGCCAGCGTCTGGCAACGCGTGTGTCATGCTCGCCTCGT 179

Qy 123 GGTGACAGAACTTAGACATCGAGTAATATTTTCTTAATTTGGCTATTTCTGA 182
Db 180 GCGGACTCGAGCTCCGACCCAGAACAACTTCTCTGCTCAACCTCGCATCTCGGA 239

Qy 183 CTTCCTCGTGGTTGATTTTCATTCCTGTACATCCCTCAGGTGTTG---TTTAACTG 239
Db 240 CTTCCTCGTGGCTTCTGATCCCACTGATGATACCTACCTGCTGACAGCGCGCTG 299

Qy 240 GAATTTTGGAAAGTGGAACTGCGATGTTTGGCTCAATTAAGTACTATCTTTTGTGACCGC 299
Db 300 GACCTTCGCGCGGCGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGACCTC 359

Qy 300 ATCTGCTACAAATATGTCCTCATTAGCTAGATGATGATACAGTCAAGTTCATTAATGCTGT 359
Db 360 CTCTGCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTGTCGGTCAACCGCGCT 419

Qy 360 GTCTTATAGGCTCAACACATGCGCATCATGAAGATTGTTGCTCAAAATGGTGGCTTTTG 419
Db 420 CTATACCGGCGCCAGCGGTGACACCGCGGCGAGTGGGAGATGCTGTGGTGTG 479

Qy 420 GATACGTGCTTTTGGTAAATGGCCCGCATGATTTCTGGCTTCAGAT-----TCTTGGAA 473
Db 480 GGTGCTGGCTTCTGCTGTACGACAGCCATCTGAGCTGGGAGTACCTGTTCGGGG 539

Qy 474 GAACAGCAGAACACAAAGGACTGTGACCTGGCTTTGTTACAGAGTGGTACATCTCAC 533
Db 540 CAGCTCCATCCCGAGGCGCACTGCTATGCGGAGTCTTCTTACAACTGTTCTCTCAT 599

Qy 534 CATTACAATGCTTTTGGAAATTCCTGCTTCCTGTCATCTGTCGCTTATTTCAATGTACA 593
Db 600 CACGGCTTCCACCTGGAGTTCTTTACGCGCTTCTCAGCGCTCACCTTCTTTAACCTCAG 659

Qy 594 GATTTACTGGAGCCTGTGGAGCGGTAGGGCTCTCAG 629
Db 660 CATCTACTGAACATCCAGAGCGCGACCGCGCTCCG 695

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RESULT 13
US-09-891-053-21
; Sequence 21, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo

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; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; FILE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 2050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271)...(1629)
US-09-891-053-21

Query Match      11.9%; Score 140.4; DB 4; Length 2050;
Best Local Similarity 53.6%; Pred. No. 1.1e-34;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

Qy 3 GTCGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCCTTGGCATTTT 62
Db 330 GCGCGCGCGCGCGCGCGGCTTCTCGGACCTGGACCGGCTGCTGGCGCGCT 389

Qy 63 AATGTCCTTTCATTTGCTTTGCTATAATGATGATGAGCAATGCTGTGTCATCTTAGCCTTTGT 122
Db 390 CATGGCGCTGCTCATCGTGGCCAGCGTCTGGCAACGCGTGTGTCATGCTCGCCTCGT 449

Qy 123 GGTGACAGAACTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGA 182
Db 450 GCGGACTCGAGCTCCGACCCAGAACAACTTCTTCCTGCTCAACCTCGCATCTCGGA 509

Qy 183 CTTCCTCGTGGTGTGATTTTCCATTCCTGTATACATCCCTCAGCTGTG---TTTAACTG 239
Db 510 CTTCCTCGTGGCGCTTCTGCAATCCCACTGATGATACCTACCTGCTGACAGCGCGCTG 569

Qy 240 GAATTTTGGAAAGTGGAACTGTCATGTTTGGCTCAITTAAGTACTATCTTTTGTGACCGC 299
Db 570 GACCTTCGCGCGGCGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGACCTC 629

Qy 300 ATCTGCTACAAATATTCCTCTCATTTAGCTACGATACGATACAGTCAAGTTCATTAATGCTGT 359
Db 630 CTCTGCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTGTCGGTCAACCGAGCGGT 689

Qy 360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTTTTG 419
Db 690 CTATACCGGCGCCAGCAGGCTGACACCGCGCGGAGTGGGAGATGCTGTGGTGTG 749

Qy 420 GATACGTGCTTTTGGTAAATGGCCCGCATGATTTCTGGCTTCAGAT-----TCTTGGAA 473
Db 750 GGTGCTGGCTTCTGCTGTACGACCGCATCTGAGCTGGGAGTACCTGTCGCGGG 809

Qy 474 GAACAGCAGAACACAAAGGACTGTGACCTGGCTTTGTTACAGAGTGGTACATCTCAC 533
Db 810 CAGCTCCATCCCGAGGCGCACTGCTATGCGGAGTCTTCTTACAACTGGTACTTCTCAT 869

Qy 534 CATTACAATGCTTTGGAAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACA 593
Db 870 CACGGCTTCCACCTGGAGTTCTTTAGCGCTTCTCAGCGTCACTTCTTTAACCTCAG 929

Qy 594 GATTTACTGGAGCCTGTGGAGCGGTAGGGCTCTCAG 629

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Db 930 CATCTACCTGAACATCCAGAGGCGCACCGCCTCCG 965

## RESULT 14

US-09-949-016-5059

; Sequence 5059, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5059

; LENGTH: 2665

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-5059

Query Match 11.9%; Score 140.4; DB 4; Length 2665;  
Best Local Similarity 53.6%; Pred. No. 1.3e-34;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

QY 3 GTCGGAGTCTAACAGTACTGGCATCTTGCCACACAGCTGCTCAGGTCCCTTGGCATTTT 62

Db 351 GCGCGCGCGCGCGCGCGCGCTTCTCGGACGCTGACCGCGGTGCTGCGCGCGCT 410

QY 63 AATGCTCTTCAATTTGGCTTGTCTATATGTTAGCAATGCTGTGTCATCTTACCTTTGT 122

Db 411 CATGGCGCTGCTCATGTGGCCACGGTGTGGCAACGCGTGTGTCATGCTGCGCTTGT 470

QY 123 GGTGGACAGAACTTATAGACATCGAAGTAATATTTTCTTAAATTTGGCTATTTCTGA 182

Db 471 GCGGAGCTGAGCTCGGACCCAGAACAACTTCTTCTGCTCAACTGCGCATCTCGA 530

QY 183 CTTCTCTGCGGTTGATTTCCATTCCTGTCATACCTCAGCTGTG---TTTAACTG 239

Db 531 CTTCTCTGCGGCGCTTCTGTCATCCCACTGTATGTACCTACGCTGCTGACAGCGCGCTG 590

QY 240 GAATTTTGAAGTGAATCTGCAATGTTTGGCTCATTACTGACTATCTTTTGTGCAACGC 299

Db 591 GACCTTGGCGCGGCGCTTGGCAAGCTGTGGCTAGTGGACTACTGCTGTGACCTC 650

QY 300 ATCTGTCTACAATTTGCTCTCATAGTACGATCGATACCACTCAGTTTCAATGCTGT 359

Db 651 CTCTGCTTCAACATCGTCTCATAGTACGACCGCTTCTCTGCTGCTCAGCGCGGT 710

QY 360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAATGCTGCTGTTG 419

Db 711 CTATACCGGCGCGCAGCAGGCTGACACGCGCGGCGAGTGCAGGAAGATGCTGCTGTG 770

QY 420 GATACTGGCTTCTTGTGAATGCGCGGATGATTTCTGGCTTCAGAT-----TCTTGA 473

Db 771 GGTGTGGCGCTTCTGCTGTACGACAGCCATCTTACGCTGGAGTACTGTCGCGGG 830

QY 474 GAACAGCAGAAACACAAAGACTGTGAGCCTTGCTTTGTTTACAGAGTGGTACATCTCAC 533

Db 831 CAGCTCATCCCGAGGCGCACTGCTATGCGGAGTCTTCTCAACCTGCTGCTCAT 890

QY 534 CATTACATGCTCTTGAATTTCTGCTTCTGTCATCTCTGTCATCTCTGTCGCTTATTTCA 593

Db 891 CACGGCTTCCACCGCTGAGTCTTTTAGCGCCCTTCTCAGCGTCACCTTCTTTAACCTCAG 950

QY 594 GATTTACTGGAGCTGTGGAAGCGTAGGGCTCTCAG 629

Db 951 CATCTACCTGAACATCCAGAGGCGCACCGCCTCCG 986

## RESULT 15

US-08-985-090-1

; Sequence 1, Application US/08985090

; Patent No. 5885893

; GENERAL INFORMATION:

; APPLICANT: Andrew D.J. Goodearl

; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/985,090

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Jean M. Silveri

; REGISTRATION NUMBER: 39,030

; REFERENCE/DOCKET NUMBER: MNI-032

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2689 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 291..1625

US-08-985-090-1

Query Match 11.9%; Score 140.4; DB 2; Length 2689;  
Best Local Similarity 53.6%; Pred. No. 1.3e-34;  
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

QY 3 GTCGGAGTCTAACAGTACTGGCATCTTGCCACACAGCTGCTCAGGTCCCTTGGCATTTT 62

Db 350 GCGCGCGCGCGCGCGCGCGCTTCTCGGACGCTGACCGCGGTGCTGCGCGCGCT 409

QY 63 AATGCTTCAATTTGCTTGTCTATATGTTAGCAATGCTGTGTCATCTTACCTTTGT 122

Db 410 CATGGCGCTGCTCATGCTGGCCACGCTGCTGGGCAACGCGCTGCTGCTGCTGCT 469

QY 123 GGTGGACAGAACTTATAGACATCGAAGTAATATTTTCTTAAATTTGGCTATTTCTGA 182

Db 470 GCGGAGCTCGAGCTCCGACCCAGAACTTCTTCTGCTCACTCGCATCTCCGA 529

QY 183 CTTCTCTGCGGTTTGAATTTCCATTCCTCTGTACATCCCTCAGTGTG---TTTAACTG 239

Db 530 CTTCTCTGCGGCGCTTCTGTCATCCCACTGTATGTACCTACGCTGCTGACAGCGCGCTG 589

QY 240 GAATTTTGAAGTGAATCTGTCATGTTTGGCTCATCTACTGACTATCTTTTGTGACCGC 299

Db 590 GACCTTGGCGCGCGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGCACTC 649

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Qy 300 ATCTGTCTACAAATATTGCTCCTCAITTAGCTACGATACGATACGATTTTCAAATGCTGT 359
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 650 CTCTGCCCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGCGTCACTCGGAGCGGT 709
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 360 GTCTTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAANTGGTGGCTGTTTG 419
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 710 CTCATACCGGGCCAGCGGTGACACGGGGCGGCGAGTGGGAAAGATGCTGCTGGTGTG 769
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 420 GATACTGGCTTTCTTTGGTAAATGGCCCGATGATTCTGGCTTCAGAT-----TCTTGGAA 473
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 770 GGTGCTGGCTTCTCTGCTGTACGGACAGCCATCTGAGCTGGGAGTACCTGTCCGGGGG 829
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 474 GAACAGCAGGAACACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCCTCAC 533
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 830 CAGCTCCATCCCGAGGGCCACTGTATGCCGAGTTCTTACAACTGGTACTTCTCAT 889
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 534 CATTACAATGCTTTTGGAAATTCCTGCTTCATCTCTGTGGCTTATTCAATGTACA 593
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 890 CACGGCTTCCACCTGGAGTTCTTTACGGCCCTTCTCAGCGTCACTTCTTTAACCTCAG 949
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 594 GATTTACTGGAGCCTGTGGAAGCGTAGGGCTCTCAG 629
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 950 CATCTACCTGAACATCCAGAGGGCACCAGCGCTCCG 985
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Search completed: April 7, 2005, 01:50:09  
Job time : 242 secs



	Query Match	100.0%;	Score 1176;	DB 18;	Length 1176;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1176;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGTGGAGTCTAAACAGTACTTGGCATCTTGCCACCAGCTGCTCAGTCCCTTGGCATTTT	60		
Db	1	ATGTGGAGTCTAAACAGTACTTGGCATCTTGCCACCAGCTGCTCAGTCCCTTGGCATTT	60		
QY	61	TTAATGTCCTTCAATTTGCCCTTTCCTATATATGGTAGGCAATGCTGTGTCATCTTTAGCCTTT	120		
Db	61	TTAATGTCCTTCAATTTGCCCTTTCCTATATATGGTAGGCAATGCTGTGTCATCTTTAGCCTTT	120		

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121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180
121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180
181 GACTTCTCTGCTGGTGTGATTTCCATTCCTCTGTACATCCCTCACGTTGTTTAACTGG 240
181 GACTTCTCTGCTGGTGTGATTTCCATTCCTCTGTACATCCCTCACGTTGTTTAACTGG 240
241 AATTTTGGAAAGTGGATCTGCATGTTTGGCTCAATTAAGTATCTTTTGGTGCACCGCA 300
241 AATTTTGGAAAGTGGATCTGCATGTTTGGCTCAATTAAGTATCTTTTGGTGCACCGCA 300
301 TCTGTCTACAAATTTGCTCATTAGTAGTACGATCGATCAGTTCAGTTCCTCAATGCTGTG 360
301 TCTGTCTACAAATTTGCTCATTAGTAGTACGATCGATCAGTTCAGTTCCTCAATGCTGTG 360
361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTGG 420
361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTGG 420
421 ATACTGGCTTTCTGTGTAATGCCCGATGATTTCTGGCTTCAGATTCCTTGGAAAGACAGC 480
421 ATACTGGCTTTCTGTGTAATGCCCGATGATTTCTGGCTTCAGATTCCTTGGAAAGACAGC 480
481 ACGAACACAAAGACTGTGAGCTTGGCTTTGTTACAGAGTGTGATCCTCACCATTACA 540
481 ACGAACACAAAGACTGTGAGCTTGGCTTTGTTACAGAGTGTGATCCTCACCATTACA 540
541 ATGCTCTTGGAAATCTGCTGCTCTGCTGCTCTGCTGCTTATTTCAATGTACAGATTAC 600
541 ATGCTCTTGGAAATCTGCTGCTCTGCTGCTCTGCTGCTTATTTCAATGTACAGATTAC 600
601 TGGAGGCTGTGGAAGCTAGGGCTCTCAGTAGTGGCTTACGATCCTGATTCCTCCACT 660
601 TGGAGGCTGTGGAAGCTAGGGCTCTCAGTAGTGGCTTACGATCCTGATTCCTCCACT 660
661 ACCTCTCCAGTCTTCAGAGACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT 720
661 ACCTCTCCAGTCTTCAGAGACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT 720
721 CCTGGATTTGAAGAACTCAGCTGATCTCTGCTCAGTACAGAGTCTCGAAGAAAGACAGC 780
721 CCTGGATTTGAAGAACTCAGCTGATCTCTGCTCAGTACAGAGTCTCGAAGAAAGACAGC 780
781 ATCCTGGTGTCTTAAAGACTCATATGAACAGAGTATCATCTGCTTTCAAAGTGGGTTC 840
781 ATCCTGGTGTCTTAAAGACTCATATGAACAGAGTATCATCTGCTTTCAAAGTGGGTTC 840
841 TTCTGGGATCGAAGAGTGGAGCTTCGCAAGGAGTACGAGCTTCTCAGAGGC 900
841 TTCTGGGATCGAAGAGTGGAGCTTCGCAAGGAGTACGAGCTTCTCAGAGGC 900
901 AGAAGCTAGCAGGCTCAGTGGGCTCTCTGAGGCTTTTGGCAATTTGCTGGGCTCCA 960
901 AGAAGCTAGCAGGCTCAGTGGGCTCTCTGAGGCTTTTGGCAATTTGCTGGGCTCCA 960
961 TACTGTCTGTCAAAATGCTTTCAACTTACCCAGAACGGAAGCCGCCAAATCGGTG 1020
961 TACTGTCTGTCAAAATGCTTTCAACTTACCCAGAACGGAAGCCGCCAAATCGGTG 1020
1021 TGGTACAGATTCGCTTCTGGCTGCAATGTTCAATTCGTTGTTAAATCCCTTCTGTAC 1080
1021 TGGTACAGATTCGCTTCTGGCTGCAATGTTCAATTCGTTGTTAAATCCCTTCTGTAC 1080
1081 CCTTTGTGTACAGGGCTTTCCAGAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140
1081 CCTTTGTGTACAGGGCTTTCCAGAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140
1141 CCAGCGCTGTACAGAACCAAGTCAAGTATCTTTTGA 1176
1141 CCAGCGCTGTACAGAACCAAGTCAAGTATCTTTTGA 1176
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RESULT 2
US-10-626-445-6
; Sequence 6, Application US/10626445
; Publication NO. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-445-6

Query Match      81.5%; Score 958.4; DB 18; Length 1176;
Best Local Similarity 88.4%; Pred. No. 3.8e-291;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY      1 ATGTGGAGTCTAAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCATTT 60
DB      1 ATGTGGAGTCTAAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCATTT 60
QY      61 TTAATGTCTTCAATTTGCTTGTCTATTAATGTTAGGAATGCTGTGCTATCTTAGGCTTT 120
DB      61 TTAATGTCTTCAATTTGCTTGTCTATTAATGTTAGGAATGCTGTGCTATCTTAGGCTTT 120
QY      121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180
DB      121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180
QY      181 GACTTCTCTGCTGGTGTGATTTCCATTCCTCTGTACATCCCTCACAGCTGTTTAACTGG 240
DB      181 GACTTCTCTGCTGGTGTGATTTCCATTCCTCTGTACATCCCTCACAGCTGTTTAACTGG 240
QY      241 AATTTTGGAAAGTGGATCTGCATGTTTGGCTCAATTAAGTATCTTTTGGTGCACCGCA 300
DB      241 AATTTTGGAAAGTGGATCTGCATGTTTGGCTCAATTAAGTATCTTTTGGTGCACCGCA 300
QY      301 TCTGTCTACAAATTTGCTCATTAGTAGTACGATCGATCAGTTCAGTTCCTCAATGCTGTG 360
DB      301 TCTGTCTACAAATTTGCTCATTAGTAGTACGATCGATCAGTTCAGTTCCTCAATGCTGTG 360
QY      361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTGG 420
DB      361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTGG 420
QY      421 ATACTGGCTTTCTGTTAAATGGCCGATGATTTCTGGCTTCAGATTCCTTGGAAAGACAGC 480
DB      421 ATACTGGCTTTCTGTTAAATGGCCGATGATTTCTGGCTTCAGATTCCTTGGAAAGACAGC 480
QY      481 ACGAACACAAAGACTGTGAGCTTGGCTTTGTTACAGAGTGTGATCCTCACCATTACA 540
DB      481 ACGAACACAAAGACTGTGAGCTTGGCTTTGTTACAGAGTGTGATCCTCACCATTACA 540
QY      541 ATGCTCTTGGAAATCTGCTGCTCTGCTGCTTATTTCAATGTACAGATTAC 600
DB      541 ATGCTCTTGGAAATCTGCTGCTCTGCTGCTTATTTCAATGTACAGATTAC 600
QY      601 TGGAGGCTGTGGAAGCTAGGGCTCTCAGTAGTGGCTTACGATCCTCACCATTACA 660
DB      601 TGGAGGCTGTGGAAGCTAGGGCTCTCAGTAGTGGCTTACGATCCTCACCATTACA 660
QY      661 ACCTCTTCCAGTCTTCAGAGACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT 720
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Db 661 ACCCTCTTCAGGGGCACTGGACACTCAGCGAGAACTGGGTTGGCTGTAGGACAAGTCTT 720
Qy 721 CCTGATTTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCCCTCGAAGAAAGAGCAGC 780
Db 721 CCTGATTTAAGGAACACGAGCCGATCCCTTCATTCAGAAAGTCCACGAGGAAGAGCAGT 780
Qy 781 ATCTGGTGTCTTTAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAGTGGGTTC 840
Db 781 CTCTGGTGTCTTTAAGGACTCACATGAGCGGTAGTATCATCGCCTTCAAAGTGGGTTC 840
Qy 841 TTCTGGCCATCGGAAGTGCAGCGCTTCGCCAAAGGGAGTAGCGAGCTTCTCAGAGGC 900
Db 841 TTCTGGCCATCAGAAAGCCAGTGTCTCACCAGAGAGAGCAGTGGAGCTTCTCAGAGGC 900
Qy 901 AGGAAGCTAGCCAGCTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
Db 901 AGGAAGCTAGCCAGCTCGTAGCTCTCTCTGAGTGTCTTTGCCATTTGCTGGGCTCG 960
Qy 961 TACTGTCTGTTCAAAATTTGCTTTCAACTTACCCAGAACGGAAAGCGCCCAAAATCGGTG 1020
Db 961 TATTGCCCTGTTCAAAATTTGCTTTCAACTTATCGCAGAGGGAGCGCCCAAAATCGATT 1020
Qy 1021 TGCTACAGATTCGCTTCTGCTGCAATGGTTCAATTCGTTGTTTAATCCCTTCTGTAC 1080
Db 1021 TGCTACAGATTCGCTTCTGCTGCAATGGTTCAATTCGTTGTTTAATCCCTTCTGTAC 1080
Qy 1081 CCTTTGCTCAGAGCGGTTTTCAGAAAGCTTTCTGGAAGATACTTTGTTGTGACAAAGCAA 1140
Db 1081 CCTTTGCTCAGAGCGGTTTTCAGAAAGCTTTCTGGAAGATACTCTGTGTGACAAAGCAA 1140
Qy 1141 CCAGCGCTGTCCAGAAACAGTCACTATCTTCTTGA 1176
Db 1141 CCAGCACCTTCAGAGACCCAGTCACTATCTTCTTGA 1176
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## RESULT 3

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US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1
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Query Match 58.4%; Score 686.6; DB 9; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2.3e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTGGAGTCTAACAGTACTGGCACTTGGCCACAGCTGCTCAGGTCCTTGGCAATTT 60
Db 1 ATGCCAGATCTAATAGCACAACTCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60

Qy 61 TTAATGCTTCATTTGGCTTTGCTATTAATGTTAGGCAATGCTGTGGTCACTTACGCTTT 120
Db 61 TTTATGCTTCATTTGGCTTTGCTATTAATGTTAGGCAATGCTTTGGTCACTTTTAGCTTTT 120
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Qy 121 GTGTGGACAGAAACCTTTAGACATCGAAGTAAATTAATTTTTTCTTAATTTGGCTATTTCT 180
Db 121 GTGTGGACAGAAACCTTTAGACATCGAAGTAAATTAATTTTTTCTTAATTTGGCTATTTCT 180
Qy 181 GACTTCTCGTGGGTGTGATTTCCATCTCTCTGTACATCCCTCAGCTGTGTGTTAACTGG 240
Db 181 GACTTCTTTGTGGGTGTGATTTCCATCTCTCTGTACATCCCTCAGCTGTGTGTTAACTGG 240
Qy 241 AATTTTGAAGTGAATCTGCATGTTTTTGGGCTCAATTAAGTAAATTAATTTTTTCTTAATTT 300
Db 241 AATTTTGAAGTGAATCTGTGATTTTGGGCTCAATTAAGTAAATTAATTTTTTCTTAATTT 300
Qy 301 TCTGTCTACAATTAATGCTCTCATTAAGTACGATACGATACGATACGATACGATACGATAC 360
Db 301 TCTGTATATAACAATGCTCTCATTAAGTACGATACGATACGATACGATACGATACGATAC 360
Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGTTGCTCAAAATGGTGGCTGTGTTGG 420
Db 361 TCTTATAGGCTCAACACACTGGGCTCTTGAAGATTTGTTGCTCAAAATGGTGGCTGTGTTGG 420
Qy 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTTCTTGAAGAAACAGC 480
Db 421 GTGCTGGCTTTCTTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGTCTTTGGAAGAA 476
Qy 481 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTTACAGAGTGGTACATCTCACCACATTACA 540
Db 477 -- TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTTGCCATACA 534
Qy 541 ATGCTCTTTGAATTTCTGCTTCTGTCTCATCTCTGTGGCTTAATTTCAATGTACAGATTTAC 600
Db 535 TCATTTCTGGAAATTCGTGATCCAGTCACTCTTAGTCTGCTTAATTTCAACATGAATATTTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGGATTTCTCACT 660
Db 595 TGGAGCCTGTGGAAGCGTGGATCACTCAGTAGGTGCCAAAGCCATCTCTGGACTGACTGCT 654
Qy 661 ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTGAGGACAAAGTAAT 720
Db 655 GTCTCTTCCACACTCTGTGGACACTCATTTACAGAGTAGACTATCTTTCAAGGAGATCTCTT 714
Qy 721 CCTGATTTGAAGGAATCAGCTGTGATCTGTCTCATCTCTGTGGCTTAATTTCAATGTACAGAT 780
Db 715 TCTGCATCGACAGAAAGTTCTCTGATCTCTTTTCAATTCAGAGACAGAGAGAAAGTAGT 774
Qy 781 ATCTGTGTCTCTTAAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAGTGGGTTC 840
Db 775 CTCAATTTTCTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCAAATAGGTTTC 834
Qy 841 TTCTGGGATCGGAAGTGCAGCGCTTTCGCCAAAGGGAGTAGCGAGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATCTGTAGCTTTCACCAAGGGGAACATGTTGTAACCTGCTTAGAGCC 894
Qy 901 AGGAAGCTAGCCAGCTCAGTGGCCATCTCTCTGAGCGCTTTTGGCAATTTGCTGGGCTCCA 960
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954
Qy 961 TACTGTCTGTTCACAAATTTGCTTTCAACTTTTACCCAGAGACGGAGCCCAAAATCGGTG 1020
Db 955 TATTCTCTGTTCACAAATTTGCTTTTCAATTTTATTTCTCAGCAACAGGTCCTTAATCAGTT 1014
Qy 1021 TGGTACAGCATTTGCTTCTGGCTCAATTTGTTCAATTTGTTTAAATCCCTTCTCTGTAC 1080
Db 1015 TGGTATAGATTTGATTTTGGCTTCACTGTTTCAATTTCTTTGTCAATCTCTTTTGTAT 1074
Qy 1081 CCTTTGTGTACAGGCGTTTTCAGAGGCTTTTTCGAAGATACCTTTGTGTGACAAAGCAA 1140
Db 1075 CCATTTGTGTACAGGCGTTTTCGAAGGCTTTTTCGAAGATATTTTGTATATAAAGCAA 1134
Qy 1141 CCAGCGCTGTCCAGAAAC--CAGTCACTATCTTCTTGA 1176
Db 1135 CCTCTACCATCAACACAGTCCGTCAGTATCTTCTTAA 1173
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;; PRIOR FILING DATE: 1999-05-28  
;; PRIOR APPLICATION NUMBER: 60/137,131  
;; PRIOR FILING DATE: 1999-05-28  
;; PRIOR APPLICATION NUMBER: 60/141,448  
;; PRIOR FILING DATE: 1999-06-29  
;; PRIOR APPLICATION NUMBER: 60/156,653  
;; PRIOR FILING DATE: 1999-09-29  
;; PRIOR APPLICATION NUMBER: 60/156,633  
;; PRIOR FILING DATE: 1999-09-29  
;; PRIOR APPLICATION NUMBER: 60/156,555  
;; PRIOR FILING DATE: 1999-09-29  
;; PRIOR APPLICATION NUMBER: 60/156,634  
;; PRIOR FILING DATE: 1999-09-29  
;; PRIOR APPLICATION NUMBER: 60/157,280  
;; PRIOR FILING DATE: 1999-10-01  
;; PRIOR APPLICATION NUMBER: 60/157,294  
;; PRIOR FILING DATE: 1999-10-01  
;; PRIOR APPLICATION NUMBER: 60/157,281  
;; PRIOR FILING DATE: 1999-10-01  
;; PRIOR APPLICATION NUMBER: 60/157,293  
;; PRIOR FILING DATE: 1999-10-01  
;; PRIOR APPLICATION NUMBER: 60/157,282  
;; PRIOR FILING DATE: 1999-10-01  
;; NUMBER OF SEQ ID NOS: 74  
;; SOFTWARE: Patent in Ver. 2.1  
;; SEQ ID NO 13  
;; LENGTH: 1173  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-875-076-13

Query Match 58.4%; Score 686.6; DB 10; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 2.3e-205;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
  
Qy 1 ATGTCGGAGTCTAACAGTACTGGGCACTTGGCCACGAGTGTCTCAGGTCCTTGGCAATTT 60  
Db 1 ATGCCAGATACCTAATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60  
  
Qy 61 TTAATGTCCTCATTTGCTTTGCTATATGTTAGGCAATGCTGTGGTCATCTTAGCCCTTT 120  
Db 61 TTTATGTCCTTAGTAGCTTTTGTATATGTTAGGCAATGCTGTGGTCATCTTTAGCTTTT 120  
  
Qy 121 GTGTGGACAGAACTTAGACATCGAAAGTAATATTTTCTTAAATTTGGCTATTTCT 180  
Db 121 GTGTGGACAAACCTTAGACATCGAAGTAGTATTTTCTTAACTTGGCCATCTCT 180  
  
Qy 181 GACTTCTCGTGGGTTGATTTCCATTCCTCTGTACATCCCTCAGTGTGTTTAACTGG 240  
Db 181 GACTTCTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCAGTGTGTTTAACTGG 240  
  
Qy 241 AATTTTGAAGTGGAACTGCAATGCTTTTGGCTCATTTACTGACTATCTTTTGGCACCGCA 300  
Db 241 GATTTTGAAGAGGAATCTGTATATTTTGGCTCACTACTGACTATCTTTTGTATGACAGCA 300  
  
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Db 301 TCTGTATATACATTTGCTCTCATCAGCTATGATCGATACCTGTGCTGCTCAATGCTGTG 360  
  
Qy 361 TCTTATAGGCTCAACACACTGGCAATGATGATGTTGTTGTTCAAAATGGTGGCTGTTTGG 420  
Db 361 TCTTATAGAACTCAACATACTGGGCTCTTGAAGATTGTTACTCTGATGGTGGCGCTTGG 420  
  
Qy 421 ATACTGGCTTTCTTGGTAAGTGGCCGATGATTTGGCTTCAGATTTCTTGAAGACAGC 480  
Db 421 GTGTGGCTTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCTAGAGTCTTTGGAAGCA 476  
  
Qy 481 ACGAACAAAGGAGTGTGAGCTGGCTTTGTTTACAGAGTGTGATCATCTCACCATTACA 540  
Db 477 --TGNAGGTAGTGAATGTGAACCTGGATTTTTCGGGAATGGTATCTTGGCCATCACA 534  
  
Qy 541 ATGCTCTTGGAAATCTCTCTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600  
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Db 535 TCATTCTTGGAAATTCGTGATCCCACTCATTTAGTCGCTTATTTCAACATGAATATTTAT 594  
Qy 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCCCTAGCCATCTGCGATTTCTCCACT 660  
Db 595 TGGAGCCTGTGGAAGCGTAGATCATCTCAGTAGGTGCCCCAAGCCATCTCTGGACTGCTGCT 654  
Qy 661 ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720  
Db 655 GTCTCTTCCAACTCTGTGGACACTCATTTCAAGAGTAGACTATCTTCAAGGAGATCTCTTT 714  
Qy 721 CCTGATTTGAGGAATCAGCTGCACTCTCGTCACACAGAAAGTCTCTCGAAGAAAGAGCAGC 780  
Db 715 TCTGATCGACAGAAAGTTCTGCACTCTTTTCAATTCAGAGACAGAGAGAAAGAGTAGT 774  
Qy 781 ATCTGTGTCTTAAAGGACTCACATGAACAGCAGTATCATCTGCTTCAAAAGTGGGTTCC 840  
Db 775 CTGATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTCC 834  
Qy 841 TTCTGGGATCGGAAAGTGCAGCGCTTGCACAAAGGAGTAGTACGAGAGCTTCTCAGAGGC 900  
Db 835 TTCTCCCAATCAGATTTCTGTAGCTCTTCCACCAAGGGAACATGTTGAATCTGCTTAGAGCC 894  
Qy 901 AGGAGCTAGCCAGTCACTGGCCATCTTCTGAGCGCTTTTGGCATTTGCTGGGCTCCA 960  
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTGTGCTTGTGGGCTCCA 954  
Qy 961 TACTGTCTGTTCACAATTTGCTTTCACACTTACCCAGAACGGAACGCCCAATCGGTG 1020  
Db 955 TATTCTGTTCACAATTTGCTTTCATTTTATTTCTCAGCAACAGGTCCTTAATCAGTT 1014  
Qy 1021 TGGTACAGCATGCTTCTGGCTCAATGTTCAATGTTTAAATGTTTAAATGTTTCTGTTGAC 1080  
Db 1015 TGGTATAGAAATTCATTTTGGCTTCAAGTGTGTTCAATTCCTTGTCAATCTCTTTGTAT 1074  
Qy 1081 CCTTGTGTACAGCGCTTTCACAGAGCTTCTGGAAGATACCTTGTGTGACAAAGCAA 1140  
Db 1075 CCATTGTGTCAAGCGCTTTCAAAGGCTTCTTGAAGAAATATTTTGTATAAAAAGCAA 1134  
Qy 1141 CCAGCGTGTACAGAAAC---CAGTCAGTATCTTCTTGA 1176  
Db 1135 CCTTACATCACAAACAGCTGCTGCTAGTATCTTCTTAA 1173

RESULT 6  
US-09-876-252-13  
; Sequence 13, Application US/09876252  
; Publication No. US20030018182A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Lehmann-Bruinsma, Karin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Receptor  
; CURRENT APPLICATION NUMBER: US/09/876,252  
; CURRENT FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944

PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,945  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,948  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,951  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,946  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,949  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/152,524  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: 60/151,114  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: 60/108,029  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: 60/136,436  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,439  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,567  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/137,127  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/137,131  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/141,448  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: 60/136,437  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/156,555  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,634  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,653  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/157,280  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,294  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,281  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,282  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/156,633  
PRIOR FILING DATE: 1999-09-29  
NUMBER OF SEQ ID NOS: 146  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 13  
LENGTH: 1173  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-876-252-13

Query Match 58.4%; Score 686.6; DB 10; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 2,3e-205;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGCGAGGTCTAACAGTACTGGCACTTCCTGCCACCAAGTGCTCAGGTCCCTTTGGCATTT 60  
Dd 1 ATGCCAGATACTAATAGCAACAATTTTATCACTAAGCACTCGTGTTACTTTAGCATTT 60  
Qy 61 TTAATGTCITCATTTGCCTTTTGTATTAATGGTAGGAATGCTGGTGCATCTTAGCCCTTT 120  
Dd 61 TTTATGTCCTTAGTAGCTTTTGTATTAATGCTAGGAATGCTTTTGGTCAITTTTAGCTTT 120  
Qy 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTTTTTTTCTTAATTTTGGCTATTCT 180  
Dd 121 GTGGTGACAAAACCTTTAGACATCGAAGTAGTTATTTTTTCTTAATTTTGGCCATCTCT 180  
Qy 181 GACTTCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGCTGTGTGTTAACTGG 240

; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS

; FILE REFERENCE: PC10963A

; CURRENT APPLICATION NUMBER: US/10/052,193

; CURRENT FILING DATE: 2002-01-17

; PRIOR APPLICATION NUMBER: 0101223.6

; PRIOR FILING DATE: 2001-01-17

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-052-193-1

Query Match 58.4%; Score 686.6; DB 13; Length 1173;

Best Local Similarity 75.1%; Pred. No. 2.3e-205;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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Qy 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCTTGGCAATTT 60
Db 1 ATGCCAGATACATAAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
Qy 61 TTAATGCTCTCATTTGGCTTTGCTATATGTTAGGCAATGCTGTGGTCATCTTAGCCCTTT 120
Db 61 TTTATGCTCTTAGTACTTTTGTCTATATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT 120
Qy 121 GTGTGGACAGAAACCTTTAGACATCGAAAGTAATATTTTTTTTCTTAATTTGGCTATTTCT 180
Db 121 GTGTGGACAGAAACCTTTAGACATCGAAAGTAGTATTTTTTTTCTTAATTTGGCCATCTCT 180
Qy 181 GACTTCTCTGGGTTTGAATTTCCATCTCTGTACATCCCTCAGGTGTTGTTAACTGG 240
Db 181 GACTTCTCTGGGTTGATCTCAATCTCTTTGTACATCCCTCAGCTGTTCGAATGG 240
Qy 241 AATTTTGAAGTGAATCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGACCGCA 300
Db 241 GATTTTGAAGGAATCTGTGATTTTGGCTCACTGACTATCTGTTATGTATACAGCA 300
Qy 301 TCTGTACAAATATTTGCTCTCAATAGTACATCGATACCACTCAGTTTCAATAGCTGTG 360
Db 301 TCTGTATACATTTGCTCTCATCAGCTATGATCGATACCTGTGACTCAATAGCTGTG 360
Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGTGCTCAAAATGGTGGCTTTGG 420
Db 361 TCTTATAGAACTCAACATACCTGGGCTCTGAAGATTTGTACTCTGATGGTGGCTTTGG 420
Qy 421 ATATGCTCTTCTTGGTAAATGGCCGATGATCTGGCTTCAGATTTCTGGAAGACAGC 480
Db 421 GTCTGGCTCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGAAGGA 476
Qy 481 ACGAACACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCACCATTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGTACATCTTGGCATACA 534
Qy 541 ATGCTCTTGAATTTCTGCTTCTGTGTCATCTCTGTGGCTTTATTTCAATGTACAGATTTAC 600
Db 535 TCATTTCTTGAATTTCTGTGATCCAGTCACTCTAGTGGCTTTATTTCAACATGAATATTAT 594
Qy 601 TGGAGCTGTGGAAGCTGAGGCTCTCAGTAGGTGCTTACCCATGCTGGATTTCTCACT 660
Db 595 TGGAGCTGTGGAAGCTGAGTCACTCTCAGTAGGTGCTTACCCATGCTGGACTCACTGCT 654
Qy 661 ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACCAAGTAAT 720
Db 655 GTCTCTTCCACATCTCTGGGACATCTATTGAGAGTAGACTATCTTCAAGAGATCTCTT 714
Qy 721 CCTGGAATGAAGGAATCAGCTGTCATCTGTGTCATCTCTGTGGCTTTATTTCAATGTACAGATTTAC 780
Db 715 TCTGCATCGACAGAAAGTTCCTGTCATCTCTTTCATTTCAAGAGACAGAGAGAGAGTAGT 774
Qy 781 ATCTGTGTGCTTAAAGGACTCAATGACAGAGATATCACTGCTTCAAAAGTGGGTTC 840
Db 775 CTCAATGTTTTCTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGGTTC 834

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RESULT 8

US-10-272-983-13

; Sequence 13, Application US/10272983

; Publication No. US20030148450A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Ruoping

; APPLICANT: Dang, Huong T.

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

; FILE REFERENCE: AREN0050

; CURRENT APPLICATION NUMBER: US/10/272,983

; CURRENT FILING DATE: 2002-10-17

; PRIOR APPLICATION NUMBER: US/09/417,044

; PRIOR FILING DATE: 1999-10-12

; PRIOR APPLICATION NUMBER: 60/109,213

; PRIOR FILING DATE: 1998-11-20

; PRIOR APPLICATION NUMBER: 60/120,416

; PRIOR FILING DATE: 1999-02-16

; PRIOR APPLICATION NUMBER: 60/121,851

; PRIOR FILING DATE: 1999-02-26

; PRIOR APPLICATION NUMBER: 60/123,946

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/123,949

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/136,436

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/136,437

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/136,439

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/136,567

; PRIOR FILING DATE: 1999-05-28

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-272-983-13

Query Match 58.4%; Score 686.6; DB 15; Length 1173;

Best Local Similarity 75.1%; Pred. No. 2.3e-205;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCTTGGCAATTT 60

Db 1 ATCCGAGTACTAATAGCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
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 Db 61 TTTATGTCCTTCAATGCTTGGCTTGTCTAATAAGTGAAGCAATGCTGTGTCATCTTAGCGTTT 120  
 QY 121 GTGGTGGAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTCTT 180  
 Db 121 GTGGTGGAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTCTT 180  
 QY 181 GACTTCTCTGCTGGGTTGATTTCCATTCCTCTGTACATCCCTCACAGCTGTTTCAACTGG 240  
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 QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGGTGGCTGTTTGG 420  
 Db 361 TCTTATAGAACTCAACACTGGCATCATGAAGATTTGCTCAAAATGGTGGCTGTTTGG 420  
 QY 421 ATACTGGCTTCTTGTGAATGGCCGATGATTTCTGGCTTCAAGATTTCTTGGAGAACAGC 480  
 Db 421 GTGCTGGCTTCTTGTGAATGGCCGATGATTTCTGGCTTCAAGATTTCTTGGAGAACAGC 480  
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 Db 595 TGGAGGCTGTGGAAGGTGAGTCTCAGTAGTGCTTGTAGTGGCTTGTAGTGGCTTGTAGT 654  
 QY 661 ACCTCTTCCAGTCTTCCAGACACTTACACAGAGCTGGGTTGGCTTGCAGGACAGTAAT 720  
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 Db 775 CTATGTTTTCTCAAGAACCAAGATGATAGCAATACAAATTCCTTCCAAATGGGTTC 834  
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 Db 895 AGGAGATTAGCAAGTCACTGGGCTTCTCTTGGGCTTTTGTGTTGTGGGCTTCA 954  
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 Db 1135 CCTTACCATTCAACACACAGTCGGTCAGTATCTTCTTAA 1173  
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 ; Sequence 1, Application US/10354769  
 ; Publication No. US20030149242A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pfizer Inc.  
 ; APPLICANT: O'Reilly, Mark A.  
 ; APPLICANT: Peter, Beate  
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDE  
 ; FILE REFERENCE: PC10373B  
 ; CURRENT APPLICATION NUMBER: US/10/354,769  
 ; CURRENT FILING DATE: 2003-01-30  
 ; PRIOR APPLICATION NUMBER: US 09/698,801  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/211,243  
 ; PRIOR FILING DATE: 2000-06-14  
 ; PRIOR APPLICATION NUMBER: GB 9925641.4  
 ; PRIOR FILING DATE: 1999-10-29  
 ; PRIOR APPLICATION NUMBER: GB 0009973.9  
 ; PRIOR FILING DATE: 2000-04-20  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1173  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-354-769-1  
 Query Match 58.4%; Score 686.6; DB 15; Length 1173;  
 Best Local Similarity 75.1%; Pred. No. 2.3e-205;  
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
 QY 1 ATGTGCGAGCTAAACAGTACTGGCATCTTGGCCACAGCTGCTCAGTCCCTTGGCATTT 60  
 Db 1 ATGCCAGATACATAATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
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 QY 301 TCTGTCTACAAATTTGCTCATTAGTACGATCGATCGATCGATCGATCGATCGATCGATCG 360  
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 QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGGTGGCTGTTTGG 420  
 Db 361 TCTTATAGAACTCAACACTGGCATCATGAAGATTTGCTCAAAATGGTGGCTGTTTGG 420  
 QY 421 ATACTGGCTTCTTGTGAATGGCCGATGATTTCTGGCTTCAAGATTTCTTGGAGAACAGC 480  
 Db 421 GTGCTGGCTTCTTGTGAATGGCCGATGATTTCTGGCTTCAAGATTTCTTGGAGAACAGC 480  
 QY 481 ACGAACAACAAGGAGTGTGAGGCTGGCTTTGTGTACAGTGGGTACATCTCCACCATTTACA 540



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Qy 601 TGGAGCCTGTGGAAGCGTAGGCTCTCAGTAGGTGCTTACCTAGCTGCTGGAATCTTCACT 660
Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAGCCATCTCTGGACTGACTGCT 654
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Db 655 GTCTCTTCCACATCTGTGGACATCTATTCAGAGTAGACTATCTTCAAGAGATCTCTT 714
Qy 721 CCTGATTTGAAGGAATCAGCTGCTATCTGTCATCTCAGAAAGTCTTCGAAAGAAAGCAGC 780
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Qy 781 ATCTGTGTCTTGAAGACTCACATGAACAGCAGTATCATCTGCTTCAAAAGTGGGTTC 840
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Qy 841 TTCTGGCATCGGAAGTGCAGCGCTTCGCCAAGGGAGTAGCGAGAGCTTCTCAGAGGC 900
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Db 1075 CCATTTGTGTACAGCGCTTTCAGAAAGCTTTCTGGAAGATATTTGTATAAAGGCAA 1134
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RESULT 10

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US-10-393-807-13
; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
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; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-393-807-13
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Query Match 58.4%; Score 686.6; DB 16; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2.3e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCCTTGGCAATTT 60
Db 1 ATGCCAGATCTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
Qy 61 TTAATGTCTTCATTTGCTTTGCTTAAATGTTAGGCAATGCTGTGGTCACTCTTAGCCCTTT 120
Db 61 TTTATGTCTCTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120
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Db 121 GTGTGTGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAATTTGGCCATCTCT 180
Qy 181 GACTTCTCTGCTGGGTTTGAATTTCCATCTCTGTACATCCCTCAGCTGTTGTTAACTGG 240
Db 181 GACTTCTTGTGGGTGTGATCTCCATCTCTTGTACATCCCTCAGCTGTTGCGAATGG 240
Qy 241 AATTTTGGAGTGGAAATCTGCAATGTTTGGCTCAATTAATGCTATCTTTTGTGCAACCGA 300
Db 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
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Db 301 TCTGTATATACATTTGCTCCTCATCAGCTATGATGATGATGATGATGATGATGATGATG 360
Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGCTCAAAATGGTGGCTGTTTGG 420
Db 361 TCTTATAGAACTCAACATCTGGGCTCTTGAAGATTTGTTACTCTGATGGTGGCCGCTTGG 420
Qy 421 ATACTGGCTTTCTTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAGC 480
Db 421 GTGCTGGCTTCTTTAGTGAATGGGCCAATGATTTCTAGTTTCTAGAGTCTTGGAAAGCA --- 476
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Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTTCGGAATGGTATCATCTTGGCCATACA 534
Qy 541 ATGCTCTTGGAAATTCCTGCTTCTCTGCTCATCTCTGCTGCTTATTTCAATGTACAGATTTAC 600
Db 535 TCATTTCTTGGAAATTCGTTGATCCCGATCTATCTAGTCTGCTTATTTCAACATGAATATTTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTAGGCTCTCAGTAGGTGCTTACCTAGCTGCTTCCCTTCCACT 660
Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAGCCATCTCTGGACTGACTGCT 654
Qy 661 ACCTCTTCCAGTGCTTCAGGACACATTCACAGAGCTGGGGTGGCTTGCAGAGCAAGTAAT 720
Db 655 GTCTCTTCCACATCTCTGTGGACATCTCAATCAGAGGTAGACTATCTTCAAGAGAGATCTCTT 714
Qy 721 CCTGATTTGAAGGAATCAGCTGCTATCTGTCATCTCAGAAAGTCTCTCGAAGAAAGAGCAGC 780
Db 715 TCTGCATCGACAGAGTTCTCTGCTATCTTTCAATTCAGAGACAGAGAGAGAGTAGT 774
Qy 781 ATCTGTGTCTTTAAGGACTCACATGAACAGCAGTATCATCTGCTTCTTCAAAAGTGGTTC 840
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Db 1015 TGGTATAGAAATTCAGATTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTTGTAT 1074  
Qy 1081 CTTTGTGTACAGCGTTTCAGAGGCTTTTCGGAAGATACCTTTGTGTGACAAAGCAA 1140  
Db 1075 CCATTGTGTACAGCGCTTTCAAAGGCTTTCTTGAAATATTTTGTATATAAAGCAA 1134  
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RESULT 12

US-10-349-253A-1  
; Sequence 1, Application US/10349253A  
; Publication No. US20040043393A1  
; GENERAL INFORMATION:  
; APPLICANT: Aubart, Kelly  
; APPLICANT: Bergsma, Derk  
; APPLICANT: Fitzgerald, Laura  
; APPLICANT: Graybill, Todd  
; APPLICANT: Li, Xiatong  
; APPLICANT: Michalovich, David  
; APPLICANT: Morrow, Dwight  
; APPLICANT: Zhu, Yuan  
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor  
; FILE REFERENCE: GP70655-2C2  
; CURRENT APPLICATION NUMBER: US/10/349,253A  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 09/910,411  
; PRIOR FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: 09/693,761  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/497,790  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/431,898  
; PRIOR FILING DATE: 1999-11-02  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-349-253A-1

Query Match 58.4%; Score 686.6; DB 17; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 2.3e-205;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
Qy 1 ATGTCGGAGTCTAACAGTACTGGGATCTTGGCAACAGCTGCTCAGGTCCTTGGCATTT 60  
Db 1 ATGCCAGATCTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
Qy 61 TTAATGCTCTCATTTGCTTTGCTATATGCTAGGCAATGCTGTTGCTATCTTAGCCTTT 120  
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Db 181 GACTTCTTGTGGGTGTCATCTCCATCTCTTGTACATCCCTCAGCTGTTTGAATGG 240  
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Db 361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTTGTTACTCTGATGGTGGCCCTTTGG 420  
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RESULT 13

US-10-723-955-13  
; Sequence 13, Application US/10723955  
; Publication No. US20040110238A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lehman-Bruinema, Karin  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Gore, Martin  
; APPLICANT: White, Carol  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors



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; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-782-596-13

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Best Local Similarity 75.1%; Pred. No. 2.3e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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Qy 661 ACCTCTTCCAGTCTCAGGACATCTACAGAGCTGGGGTGGCTTGCAGGACCAAGTAAT 720
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RESULT 15
US-10-737-619-1
; Sequence 1, Application US/10737619
; Publication No. US20040138234A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PCI0963A
; CURRENT APPLICATION NUMBER: US/10737,619
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-737-619-1

Query Match      58.4%; Score 686.6; DB 18; Length 1173;
Best Local Similarity 75.1%; Pred. No. 2.3e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCTTGGCAATTT 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 TTAATGCTCTTCAATTTGGCTTTGCTATAATGGTAGGCAATGCTGTGGTCAATCTTACGCTTT 120
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Qy 61 TTAATGCTCTTCAATTTGGCTTTGCTATAATGGTAGGCAATGCTGTGGTCAATCTTACGCTTT 120
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Qy 121 GTGTGGAGCAAGAACCTTAGACATCGAAGTAAATTTATTTTCTTAAATTTGGCTATTCT 180
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Qy 121 GTGTGGAGCAAGAACCTTAGACATCGAAGTAAATTTATTTTCTTAAATTTGGCTATTCT 180
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Qy 181 GACTTCTCTGGGTTTGAATTTCCATTCCTGTGTACATCCCTCACGCTGTTTAACTGG 240
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Qy 181 GACTTCTCTGGGTTTGAATTTCCATTCCTGTGTACATCCCTCACGCTGTTTAACTGG 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 AATTTTGGAGAGTGAATCTGCAATGTTTGGCTCAATTAATCTATCTTTTGTGTCACCGCA 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 AATTTTGGAGAGTGAATCTGCAATGTTTGGCTCAATTAATCTATCTTTTGTGTCACCGCA 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 477 -TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534
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Qy 541 ATGCTCTTGGAAATTCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 721 CCTGGATGAAGGAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
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Qy 715 TCTGCATCGACAGAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774
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Qy 781 ATCTGTGTCTTAAAGACTCAGATGAACAGCAGTATCACTGCTCTCAAGTGGGTTC 840
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAATGGGTTC 834
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 22:32:52 ; Search time 4423 Seconds  
(without alignments)  
10120.638 Million cell updates/sec

Title: US-10-626-445-5

Perfect score: 1176

Sequence: 1 atgtcggagtctaacagtac.....accagtcagtattcttga 1176

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gse1:\*

9: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	258	21.9	721	7	CO959034
4	135.8	11.5	672	6	CB556920
5	133.8	11.4	732	7	CF147822
6	129.2	11.0	853	6	CD326085
7	115.6	9.8	684	9	CC481311
8	99	8.4	643	1	AL848045
9	96.2	8.2	716	7	CM423054
10	95.6	8.1	499	2	BF567596
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18	77.6	6.6	727	7	CR366545
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22	75.8	6.4	633	4	BJ763892
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26	74.2	6.3	697	5	BU446363	BU446363	603213444	
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30	73.4	6.2	602	1	AU207762	AU207762	AU207762	
c	31	73.2	6.2	597	4	BM355525	BM355525	rt-26a12.y
32	72.6	6.2	946	5	BQ068856	BQ068856	AGENCOURT	
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## ALIGNMENTS

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DEFINITION DKFZp781C0629\_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone  
ACCESSION BX643713  
VERSION BX643713.1 GI:34478046  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 839)  
AUTHORS Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.  
TITLE EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS  
MIPS Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp781C0629) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
LOCATION/Qualifiers  
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FEATURES  
source  
1. 839  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="DKFZp781C0629"  
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/note="Vector: pSport1\_Sfi; Site\_1: SfiIA; Site\_2: SfiIB; cDNA-collection"

ORIGIN  
Query Match 37.3%; Score 438.6; DB 5; Length 839;  
Best Local Similarity 75.9%; Pred. No. 2.6e-118;  
Matches 570; Conservative 0; Mismatches 174; Indels 7; Gaps 2;  
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Db 809 TCTGCATCGACAGAAGTCTCTGCATCTTTC 839

RESULT 2
CF147821
LOCUS
DEFINITION
IMAGE:6971900 5', mRNA sequence.
CF147821
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 704)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
```

Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Cloned through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: IRB102 row: b column: 07  
High quality sequence stop: 685.  
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/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',  
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
Please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearrayed\_plates/IRB1.preSV.dat  
a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 36.3%; Score 426.4; DB 7; Length 704;  
Best Local Similarity 77.0%; Pred. No. 1e-114;  
Matches 547; Conservative 0; Mismatches 156; Indels 7; Gaps 2;  
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Db 1 GCCAGATATAATAGCACAAATCAATTTATCAAGCACTCGTGTACTTTAGCATTTT 60  
Qy 63 AATGCTCTCATTTGCTTTGCTTATATGATGAGCAATGCTGTGCTCATCTTAGCCCTTTGT 122  
Db 61 TAGTCTCTTAGTAGCTTTTGTCTATATGCTAGAAATGCTTTGGTCATTTTAGCTTTGT 120  
Qy 123 GGTGACAGAAACCTTAGACATCGAAGTAAATTTTCTTAATTTGGCTATTTCTGA 182  
Db 121 GGTGACAGAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCTATTTCTGA 180  
Qy 183 CTTCTCTGGGTTTGAATTTCCATTTCTCTGTACATCCCTCAGCTGTTGTTAACTGGAA 242  
Db 181 CTTCTTTGGGTTGATCTCCATTTCTTTGTACATCCCTCAGCTGTTGGAATGGGA 240  
Qy 243 TTTTGGAGTGGAAATCTGCATGCTTTTGGCTCAATTAAGTATCTTTTCTGACCCGATC 302  
Db 241 TTTTGGAGGAAATCTGTGTAATTTGGCTCACTGACTATCTGTTATGTATGACAGATC 300  
Qy 303 TGTCTACAATATGCTCTCATTTAGCTACGATCCGATACAGTCCAGTTCAGATTCGTGTGTC 362  
Db 301 TGTATATAACATTTGCTTCATCATGATGATGATGATGATGATGATGATGATGATGATG 360  
Qy 363 TTATAGGCTCAACACACTGGGCATCATGAAGTATTTGTTGCTCAAAATGGTGGCTTTGGAT 422  
Db 361 TTATAGAACTCAACATACTAGGGGTCTTGAAGATTTGTTACTCTCATGCTGGTGGCTTTGGGT 420  
Qy 423 ACTGGCTTTCTTGGTAAATGGCCGATGATTTGCTGCTTCAAGTTCAGATTTCTTGAAGAACAGCAC 482  
Db 421 GCTGGCTTTCTTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGAAGAA----- 474  
Qy 483 GAAACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACAAAT 542  
Db 475 TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGATGATGATGATGATGATGATG 534  
Qy 543 GCTCTTGAATTTCTGCTTCTGTGATCATCTCTGCTGCTTATTTCAATGTACAGATTTACTG 602  
Db 535 ATTCTTGAATTCGTGATGCCAGTCACTCTTAGTCGCTTATTTCAACATGAATATTTATTG 594



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Qy 603 GAGCCTGTGGAGCGCTAGGGCTCTCAGTAGTGGCCCTAGCCATGCTGGATTCTCCACTAC 662
Db 595 GAGCCTGTGGAGCGCTAGTATCATCTCAGTAGTGGCCCAAGCCATCTCGGACTGACTGCTGT 654
Qy 663 CTCCTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTCAGGA 712
Db 655 CTCCTCCACATC-TGTGGACACTCATTCAGAGGTAGACTATCTTTTCAGGA 703

RESULT 3
CO959034
LOCUS AGENCOURT_30842625 NIH_MGC_146 Homo sapiens cDNA clone
DEFINITION IMAGE:7389774 5', mRNA sequence.
ACCESSION CO959034
VERSION CO959034.1 GI:51323616
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 721)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.llnl.gov
Plate: IRB18 row: a column: 04
High quality sequence start: 2
High quality sequence stop: 328.
FEATURES
Location/Qualifiers
source
1..721
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:7389774"
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/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_146"
/note="Vector: pCDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov/image.rearrayed_plates/IRB18.presv.dat
a. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 21.9%; Score 258; DB 7; Length 721;
Best Local Similarity 78.4%; Pred. No. 9.8e-65;
Matches 309; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 ATGTCGAGTCTACAGTACTGGCATCTTGGCCACAGCTGCTCAGTCCCTTGGCATTT 60
Db 22 ATGCAGATACCTAATAGCACAACTAATTTATCATCAAGCACTCGTGTACTTTAGCATTT 81
Qy 61 TTAATGCTCTCATTTGGCTTTGCTATAATGGTAGGCAATGCTGTGTCATCTTAGCCCTTT 120
Db 82 TTTATGCTCTTAGTAGCTTTTGGCTATAATGCTAGGAATGCTTTGGTCATTTAGCTTTT 141
Qy 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTTTCTTAATTTGGCTATTCT 180

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Db 142 GTGGTGGACAAAACCTTAGACATCGAAGTAGTTATTTTTTTCTTAACCTGGCCATCTCT 201
Qy 181 GACTTCTCTCGTGGGTTTGATTTCCATTCTCTGTACATCCCTCAGCTGTTGTTAACTGG 240
Db 202 GACTTCTTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCAGACGCTGTTGCAATGG~261
Qy 241 AATTTTGAAGTGAATCTGCATGTTTTGGCTCACTACTGACTATCTTTTTGTGCAACGCA 300
Db 262 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACCGCA 321
Qy 301 TCTGTCTACATATTTCTCTCATAGCTACCATCGATACCATGCTAGTTTCAATGCTGTG 360
Db 322 GCTGTATATAAGATTGTCTCATCAGCTATGATAAATACCTGTCAATCTCAATGCTTTG 381
Qy 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGA 394
Db 382 TCTTATGGAACGCAAAAACGGGGGCGCTGAAGA 415

RESULT 4
CO9556920
LOCUS AMGNNUC:URGP1-00001-D6-A urgp1 (14349) Rattus norvegicus cDNA clone
DEFINITION urgp1-00001-d6 5', mRNA sequence.
ACCESSION CO9556920
VERSION CO9556920.1 GI:29496320
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 672)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00001 row: d column: 6.
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Location/Qualifiers
source
1..672
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone_lib="urp1-00001-d6"
/note="Vector: pSPORT1; Rat GPCR library rearrayed
internal pSPORT vector"

ORIGIN
Query Match 11.5%; Score 135.8; DB 6; Length 672;
Best Local Similarity 57.2%; Pred. No. 1.8e-28;
Matches 267; Conservative 0; Mismatches 197; Indels 3; Gaps 1;

Qy 3 GTCCGAGTCTAACAGTACTGGCATCTTGCCACACAGCTGCTCAGGTCCCTTTGGCATTTT 62
Db 178 GCGCGCTGCAGCGGGCGCGGCTTCTCGGCTGCGCTGGACCGCTGTCTTGGCTGCCCT 237
Qy 63 AATGCTCTCATTTTGCCTTTTGTCTATAATGGTAGGCAATGCTGTGGTCACTTTAGCCTTTGT 122
Db 238 CATGCGCTGCTCATCTGTGGCCACAGTACTTGGGCAACGGCTGTGTCATGCTCGCCTTGT 297
Qy 123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTTTCTTAATTTGGCTATTTCTGA 182
Db 298 GCGGATTCGAGCTCGCGCACCCAGAACAACTCTTCTGCTCAACCTCGCCATCTCGGA 357
Qy 183 CTTCCCTCGTGGTGTGATTTCCATTCTCTGTACATCCCTCAGCTGTTGTTTAAAC---TG 239
Db 358 CTTCCCTCGTGGTGCCTTCTGTCATCCCATTTGTACGTACCTTATGTGTGACCGGCGGTG 417

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QY 240 GAATTTTGAAGTGAATCTGCAATGTTTGGCTCAATTAAGTACTATCTTTTGTGACCGC 299
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 GACCTTCGGCGGGCTCTGCAAGCTGTGGCTGGTGTAGACTACTACTGTGTGCTC 477
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 300 ATCTGTCTCAATATTGCTCTATTAGTACGATCAGATCCAGTCTGTTTCAAAATGCTGT 359
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 CTCGGTCTTCAACATCGTACTCATGCTATGATGACCGATTCTCTGAGTCACTCGAGCTGT 537
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 GTCTTATAGGCTCAACACTGGCATCATGAAGATTGTTGCTCAATAGTGGCTGTTTG 419
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 CTCTACAGGGGCCAGAGGGGACACAGACGGCGCTTCGGAAGATGACATGCTGTGTG 597
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 420 GATACCTGGCTTCTTGTAAATGGCCGATGATTTCTGGCTTCAGATT 466
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 GGTGCTGGCTTCTGCTATGGGCTGCCATCTGAGTTGGAGT 644
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
CF147822 732 bp mRNA linear EST 25-JUL-2003
LOCUS AGENCOURT_14740187 NIH_MGC_145 Homo sapiens cDNA clone
DEFINITION IMAGE:6971899 5', mRNA sequence.
ACCESSION CF147822
VERSION CF147822.1 GI:33244090
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 732)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgi.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB102 row: b column: 06
High quality sequence stop: 610.
FEATURES
source
1. .732
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971899"
/tissue_type="mixed"
/lab_host="DH10B"
/notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match 11.4%; Score 133.8; DB 7; Length 732;
Best Local Similarity 53.5%; Pred. No. 7.3e-28;
Matches 329; Conservative 0; Mismatches 277; Indels 9; Gaps 2;
QY 3 GTCGGAGTCTAAGTACTGGCATCTTGCACACAGCTGCTCAGGTCCCTTGGCAATTTT 62
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Db 76 GGCGCGCGCGGGCGCGCGGGCTTCTCGGCAGCGCTGGACCGCGTCTGCGCCGCGCT 135
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 AATGCTTTCATTTGCTTGTCTAATAATGTAAGCAATGCTGTGTCATCTTAGCCCTTTGT 122
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 136 CATGGCGTGTCTATCGTGGCCACGGTGTGGGCAACGCGTGGTCACTGCGCTTCGT 195
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 123 GGTGGACAGAAACCTTTAGACATCGAAGTAATTTATTTTCTTTAAATTTGGCTATTCTGA 182
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 196 GCGCGACTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACTCGCCATCTCCGA 255
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 183 CTTCTCTGCGGTGTAATTTCCATTCCTCTGTACATCCCTCAGTGTG---TTTAACTG 239
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 256 CTTCTCTGCGCGGCTTCTGCACTCCCACTGATGTACCTACGTCTGACAGCGCGCTG 315
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 240 GAATTTTGAAGTGGAACTGCAATGTTTGGCTCATTACTGACTATCTTTTGTGACCGC 299
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 GACCTTCGGCGCGGGGCTCTGCAAGCTGTGGTGTAGTGGACTACCTGCTGTGCACCTC 375
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 300 ATCTGTCTACAATAATTTGCTCTCAATAGCTACATCGATACCACTAGTTTCAAAATGCTGT 359
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Db 376 CTCGCTCTCAACATCGTGTCTCATAGCTACGACCGCTTCTGTGCTCACCAGCGGT 435
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTTG 419
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Db 436 CTCATACCGGCGCCAGAGGGTGACACGCGCGGCGAGTGGCGAAGATGCTGCTGTGTG 495
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QY 420 GATACCTGGCTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGA-----TTCTTGGAA 473
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 474 GAACAGACGAAACACAAAGGACTGTGAGCTGGCTTTGTACAGAGTGGTATCCTCTAC 533
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Db 556 CAGCTCCATCCCGAGGGCCACTGTGTATGCCAGTCTTCTACAACTGGTACTTCTTCAT 615
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QY 534 CATTACAAATGCTTTGGAAATTCCTGCTTCTCTCATCTCTGTGGCTATTCAATGTACA 593
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Db 616 CACGGCTTCCACACTGGAGTCTTTACGCGCCCTTCTCAGCGTCACTTTCTTTAACTCAC 675
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QY 594 GATTTACTGGAGCT 608
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Db 676 CATCTACTGGAACAT 690
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RESULT 6
CD326085 853 bp mRNA linear EST 28-MAY-2003
LOCUS AGENCOURT_14163426 NICHD_XGC_Eyel Xenopus laevis cDNA clone
DEFINITION IMAGE:6949081 5', mRNA sequence.
ACCESSION CD326085
VERSION CD326085.1 GI:31090416
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
REFERENCE 1 (bases 1 to 853)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-r@mail.nih.gov
Tissue Procurement:
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14564 row: f column: 24
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High quality sequence stop: 707.  
 Location/Qualifiers  
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 /clone="IMAGE:6949081"  
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 /lab\_host="DH108 (phage-resistant)"  
 /clone\_lib="NICHD\_XGC Eye1"  
 Note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: oligo dt.  
 Average insert size 2.3 kb. Constructed by Life  
 Technologies. Note: This is a Xenopus Gene Collection  
 (XGC) library."

ORIGIN  
 Query Match 11.0%; Score 129.2; DB 6; Length 853;  
 Best Local Similarity 58.7%; Pred. No. 1.8e-26;  
 Matches 243; Conservative 0; Mismatches 168; Indels 3; Gaps 1;  
 45 GGTCCCTGGGCAATTTTAAATGCTTTCATTTGCTTTCCTTTGCTATAATGGTAGCAATGCTGT 104  
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 381 GGTCTTCTGGTGTCTCTGATGGGGTCTCATAGTTAGCACCGTGTGGGGAATGCCCT 440  
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 105 GGTCACTTAGCTTTGGTGGGAGAGAACTTAGACATCGAAGTAATTTTCTTCT 164  
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 441 GGTCACTGGCTTTTGTGTGGACTCCAGCCCTCCGAAACCCAGATAATTTCTCTTCT 500  
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 165 TAAATTTGCTATTTCTGACTTCTCTGCTGGTGTGATTTTCCATCTCTGTATACCTCTCA 224  
 |||||  
 501 CAACCTGGCTATCTCAGATTTCTTTGTAGGTGCCCTGTGTCATCCCTCTGTATGTGCCATA 560  
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 225 CGTGTGTGTTT---AACTGGAATTTTGGAAATGGAATCTGCAATGTTTGGCTCATTAATGA 281  
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 561 CGTACTGATGGCAGATGGAGCTTTGGCAGGAGCGTTTGCAACTGTGGCTGTCTGGA 620  
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 282 CTATCTTTTGGCACCGCATCTGTCTACAATATTGCTCTCATATTAGCTACGATCGATACCA 341  
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 621 TTATCTGCTGTGACCTCGTCCGTGTTCAACATCGTCTCATCTAGCTACGACAGGTTCAT 680  
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 342 GTCAGTTTCAATAGCTGTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTC 401  
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 691 CTCTGTGACCCGGGTGTGAGTTTACCGAGCTCAGCAGAGTAACAGCCGGCATCGAGTCTT 740  
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 402 TCAATGTGGTGTGTGGATCTGGCTTTCTTGTGTAATGCGCCGATGATTCT 455  
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 741 GAAATGACCATGGTGGATCTGGCTTTCTCTATATGACCGACCATTAAT 794  
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RESULT 7  
 CC481311 684 bp DNA linear GSS 16-JUN-2003  
 LOCUS CH240\_309C10.T7 CHORI-240 Bos taurus genomic clone CH240\_309C10,  
 genomic survey sequence.  
 CC481311  
 CC481311.1 GI:31760574  
 GSS.  
 Bos taurus (cow)  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 684)  
 Holt, R., Stott, J., Yang, G., Barber, S., Smalhus, D., Prabhu, A.-L.,  
 Tsai, M., Cloutier, A., Lee, D., Girm, N., Olson, T., Mayo, M.,  
 Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,  
 Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,  
 Schein, J., Maria, M., de Jong, P., McWilliam, S., Barris, W.,  
 Dalrymple, B. P. and Telling, R.  
 Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398  
 Unpublished (2003)  
 Other\_GSSs: CH240\_309C10.TARBAC13P2

Contact: Rob Holt  
 Sequencing  
 The British Columbia Cancer Agency Genome Science Centre  
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6  
 Tel: 604-877-6085  
 Fax: 604-877-6276  
 Email: rholt@ccgsc.ca  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library  
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering-information.html). This work  
 was undertaken as part of the International Bovine BAC Mapping  
 Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the  
 British Columbia Genome Sciences Centre, Canada.  
 Seq primer: T7  
 Class: BAC ends.  
 Location/Qualifiers  
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FEATURES  
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 ORIGIN  
 Query Match 9.8%; Score 115.6; DB 9; Length 684;  
 Best Local Similarity 70.6%; Pred. No. 1.8e-22;  
 Matches 154; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
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 260 TACGTGTATATTGTTAAATCTTCTATTTTTCGCCCATCGAGTATGATTCATTCC 319  
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 210 TCTGTACATCCCTCAGCTGTTGTTTAACTGGAATTTTGGAAAGTGAATCTGCATGTTTG 269  
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 320 TTTATTATCCCTCACAGCTCTTCACTGGAGTTTGAAATAACATTTGTGCTCTTTG 379  
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 270 GCTCATTAAGTACATCTTTTGTGCGCGCATCTGTACAAATATTGCTCATTAGCTA 329  
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 380 GCTCACTACTGACTATCTTTGTGTACAGCATCTGTGTATTAACATCGTACTCATCAGCTT 439  
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 330 CGATCGATACCAGTCAGTTTCAAAATGCTGTCTTTATA 367  
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 440 TGATCGATATCAGTCAGTCTCCAATGCTGTAAGTCAAA 477  
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RESULT 8  
 AL848045 643 bp mRNA linear EST 26-NOV-2003  
 LOCUS AL848045 XGC-egg xenopus tropicalis cDNA clone TEGG022122 5', mRNA  
 sequence.  
 AL848045  
 AL848045.2 GI:38559584  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Xenopus tropicalis (western clawed frog)  
 Xenopus tropicalis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 Xenopodinae; Xenopus; Silurana.  
 1 (bases 1 to 643)  
 Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.  
 Sanger Xenopus tropicalis EST project 2001 (11\_2003)  
 Unpublished (2003)  
 On Sep 15, 2002 this sequence version replaced gi:22868310.  
 Contact: Taylor R

Sanger Institute  
Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: trop@sanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS SEQUENCE ID: TEGG02122.plkSP6  
Sequencing primer: SP6  
This sequence is from a Xenopus Gene Collection (XGC) library  
constructed by Aaron M. Zorn.  
cDNA was oligo dT primed from Sug of poly A+ RNA from egg.  
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the  
5' end and NotI at the 3' end.  
Vector: pCS107; Site 1: EcoRI; Site 2: NotI  
Host: Escherichia coli XL1-blue.

FEATURES  
source  
1..643  
/location=Qualifiers  
1..643  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
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/clone="TEGG02122"  
/dev\_stage="egg"  
/lab\_host="Escherichia coli XL1-blue"  
/clone\_lib="XGC-egg"  
/notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA  
was oligo dT primed from Sug of poly A+ RNA from egg.  
EcoRI-NotI cut cDNA was then ligated into pCS107 with  
EcoRI at the 5' end and NotI at the 3' end"

ORIGIN  
Query Match 8.4%; Score 99; DB 1; Length 643;  
Best Local Similarity 55.5%; Pred. No. 1.5e-17;  
Matches 236; Conservative 0; Mismatches 180; Indels 9; Gaps 2;  
QY 193 GGTTCATTCCTCTCTGATACCTCCCTCAGTGTGTTT---AAGTGAATTTTGA 249  
Db 83 GGTTCATTCCTCTCTGATACCTCCCTCAGTGTGTTT---AAGTGAATTTTGA 249  
QY 250 AGTGAATTCGATGTTTGGCTCATTACTGACTATCTTTTGGACCGCATCTGCTAC 309  
Db 143 AAGGCTTGGCAAGTTGGCTAGTAAAGGACTACTTTTATGCACTGCTCAGTTT 202  
QY 310 AATATTGCTCATAGTACGATACGATACAGTTCAGTTTCAAAATGCTGTCTTAGG 369  
Db 203 AATATTGCTCATAGTACGATACAGTTCATCTCAGTCACTAAAGCGGTGCTCAGA 262  
QY 370 GCTCAACACATCGGATCATGAGATTGTGCTCAATGGTGGCTGTTGGATAGTGGCT 429  
Db 263 GCACAGAAAGGAATGACAGAAATGAGTGTAAAGAAATGCTTATGTTGGTGGCAGCC 322  
QY 430 TTCTTGGTAAATGGCCCGATGATTCCTGGCTTCAGA-----TTCTTGGGAAGACAGCAG 483  
Db 323 TTCTTCTCTATGCGCCAGCATCATCCTGGGATACATGCAAGAACTACTATCTTA 382  
QY 484 AACACAAAGGACTGTGAGCGCTTGTGTGTACAGTGGTACATCCTCACCATTACAATG 543  
Db 383 CCAGAGGGGAATGTTATGAGAAATCTACTACAACTGGTATTTCTGATGATGCTTC 442  
QY 544 CTCTTGGAAATCTGCTTCTGTCATCTCTGCGCTATTTCATGTACAGATTACTGG 603  
Db 443 ACAATAGAATTTCTTACTCCATTCATCAGTGTACCTATTTCATTAAGCACTACATT 502  
QY 604 AGCCT 608  
Db 503 AACAT 507

RESULT 9  
CN423054  
LOCUS  
DEFINITION 716 bp mRNA linear EST 16-MAY-2004  
ACCESSION 1700042504731 GRN\_ES Homo sapiens cDNA 5', mRNA sequence.  
VERSION CN423054  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 716)  
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,  
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,  
Lebkowski,J and Stanton,L.W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 716 Std Error: 0.00.

FEATURES  
source  
1..716  
/location=Qualifiers  
1..716  
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/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, cell lines H1, H7, and  
H9"  
/clone\_lib="GRN ES"  
/note="oligo dT primed, full-length enriched cDNA library  
from undifferentiated hES cell lines H1 (p32), H7 (p29),  
and H9 (p26) maintained in feeder-free conditions"

ORIGIN  
Query Match 8.2%; Score 96.2; DB 7; Length 716;  
Best Local Similarity 53.8%; Pred. No. 1e-16;  
Matches 247; Conservative 0; Mismatches 203; Indels 9; Gaps 2;  
QY 180 TGACTTCTCTGCGGGTTTGATTTCATTCCTCTGTACATCCCTCAGTGTG---TTTAA 236  
Db 188 TGTCCAGCGCCAGGGCGCTTCTGCATCCCATGATGTATGTACCTAGCTGTCAGCGCG 247  
QY 237 CTGGAATTTTGAAGTGAATCTCGATGTTTGGCTCATCTACTGACTATCTTTTGTGCAC 296  
Db 248 CTGGACCTTCGCGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGATACCTGCTGTGCAC 307  
QY 297 CCACTCTGTCTACAATATTGCTCTCATAGTACGATCGATCCAGTCAAGTTTCAAATGC 356  
Db 308 CTCTCTGCTTCAACATGCTCTATCAGTACGACCCCTTCTCTGCTGCTGCTGCTGCTG 367  
QY 357 TGTGTTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGT 416  
Db 368 GGTCTCATACCGGGCCAGCAGGGTGACACGGCGGGCGAGTGGGAAGATGCTGTGGT 427  
QY 417 TTGGATCTGGCTTCTTGGTAAATGGCCCGATGATCTGGCTTCAGA-----TTCTTG 470  
Db 428 GTGGGTGCTGGCTTCTCTGCTGACGACCGCATCTCTGAGTGGGAGTACCTGTCCGG 487  
QY 471 GAAGAACACAGCAACAAAGSACTGTGAGCTGCTTGTGTACAGAGTGGTACATCCT 530  
Db 488 GGGAGCTCCATCCCGAGGGCCACTGCTATGCCGAGTCTTCTTCACACTGGTACTTCT 547  
QY 531 CACCATTAACAATGCTCTTGGAAATTCCTGCTTCTGTGTCATCTCTGTGGCTTATTTCAATGT 590  
Db 548 CATCAGGCTTCCACCTGGAGTTCTTTACGCCCTTCTCTCAGGCTCACCTTCTTTAACT 607  
QY 591 ACAGATTTACTGAGCTGTGGAAGCTAGGGCTCTCAG 629  
Db 608 CAGCATCTACTGAACATCCAGAGGGCGCACCGGCTCCG 646

RESULT 10  
BF567596  
LOCUS  
DEFINITION 499 bp mRNA linear EST 12-DEC-2000  
ACCESSION BF567596  
VERSION UI-R-B00-agr-C-06-0-UI.r1 UI-R-B00 Rattus norvegicus cDNA clone  
KEYWORDS EST.  
SOURCE UI-R-B00-agr-C-06-0-UI 5', mRNA sequence.

ACCESSION BF567596  
 VERSION BF567596.1 GI:11677326  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 499)  
 Bonaldo, M.P., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 97044477  
 8889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
 clones will be available through Research Genetics (www.resgen.com)  
 This clone is also available through the I.M.A.G.E. Consortium at  
 LLNL (info@image.llnl.gov). IMAGE ID= 1796445  
 Seq primer: M13 Forward.  
 Location/Qualifiers  
 1..499  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-B00-agr-c-06-0-UI"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="UI-R-B00"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The library  
 (UI-R-B00) is a subtracted library derived from a mixture  
 of the following tissues: thalamus, cerebellum,  
 hypothalamus, medulla, pons, midbrain, cerebral  
 corpus striatum and hippocampus. For a detailed  
 description of the library from which this clone was  
 derived, please visit our web site at  
 ratseq.eng.uiowa.edu. The subtraction has been previously  
 described in (Bonaldo, Lennon and Soares, Genome Research  
 6:791-806, 1996)."  
 ORIGIN  
 Query Match 8.1%; Score 95.6; DB 2; Length 499;  
 Best Local Similarity 54.5%; Pred. No. 1.4e-16;  
 Matches 238; Conservative 0; Mismatches 190; Indels 9; Gaps 2;  
 Qy 192 GGGTTTGAATTCCTCTGTACATCCCTCACGTGTGTTTAAAC---TGGAAATTTGG 248  
 Db 58 GGGTGCCTTCGATCCCATTTGTACCTACCTCATCTGTGCGCGCCGCTTGGACCTCG 117  
 Qy 249 AAGTGGATCTGCATGTTTGGCTCATCTACTGACTATCTTTTGGCCAGCATCTGCTA 308  
 Db 118 CCGGGGCTCTGCAAGCTGTGGCTGGTGGTAGACTACCTACTGTGTGCTCTCGGCTT 177  
 Qy 309 CAATATTCTCTCATTAGCTAGATACAGTACAGTACAGTACAGTACAGTACAGTACAG 368  
 Db 178 CAACATCTACTCATCAGCTATGACCGAATCTCTGTCAGTCACTGAGCTGTCCTACAG 237  
 Qy 369 GGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTTGGATACAT 428  
 Db 238 GGCCAGCAGGGGACACAGACGGCGCTTCGGAAGATGACACTGGGTGGTGGCTGGC 297  
 Qy 429 TTTCTTGAATAGCCCGCATGATCTCGCTTCAGA-----TTCTTGGAAAGACAGAC 482  
 Db 298 CTTCTGCTGTATGGGCTGCCATCTCTGAGTTGGAGTACCTGTCTGTGGCAGTTCCAT 357

Qy 483 GAACACAAAGGACTGTGAGCCCTGGCTTTGTTTACAGAGTGGTACATCCTCACCATTAAT 542  
 Db 358 CCCGAGGGCCACTGCTATGCTGAGTCTTCTTACAACTGGTACTTCTCATCACGNCCTC 417  
 Qy 543 GCTCTTGAATTCCTGCTTCTCTGTCATCTCTGTGGCTTATTTCATATGACAGATTACTG 602  
 Db 418 CACCTCGAGTCTTCTTACGCGCTTCTCTCAGCGTTTACCTTCTTCAACCTCAGCATCTACCT 477  
 Qy 603 GAGCTGTGGAAGCGTA 619  
 Db 478 GAACATCAGAGCGCA 494  
 RESULT 11  
 LOCUS BQ950659 1046 bp mRNA linear EST 21-AUG-2002  
 DEFINITION AGENCOURT\_863943 NIH\_MGC\_129 Mus musculus cDNA clone IMAGE:6311932  
 5', mRNA sequence.  
 ACCESSION BQ950659  
 VERSION BQ950659.1 GI:22366137  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/  
 1 (bases 1 to 1046)  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Susan L. Sullivan, PhD.  
 cDNA Library Preparation: ResGen, Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM13736 Row: k column: 05  
 High quality sequence stop: 640.  
 Location/Qualifiers  
 1..1046  
 /organism="Mus musculus"  
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 /clone="IMAGE:6311932"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;  
 Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.  
 Primer: Oligo dT. Average insert size 2.2 kb. Constructed  
 by ResGen, Invitrogen Corp. Note: this is a NIH\_MGC  
 Library."  
 ORIGIN  
 Query Match 7.5%; Score 88.6; DB 5; Length 1046;  
 Best Local Similarity 61.6%; Pred. No. 2.2e-14;  
 Matches 141; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 Qy 238 TGGAAATTTGGAAGTGGAAATCTGCATGTTTGGCTCACTACTGACTACTTCTTTTGGCACC 297  
 Db 488 TGGACCTTTGGCGGGGCTCTGCAAGCTGTGGCTGGTGGTAGACTACTACTGTGTGCC 547  
 Qy 298 GCATCTGCTCAATATTTGCTCTCATTTAGTACATGATACGATGATGATGATGATGATGAT 357  
 Db 548 TCCTCAGTCTTCAACATCGTCTGATCAGCTATGACCGATTCTCTGTCAGTCACTCGAGCT 607  
 Qy 358 GTGTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGTTGCTGCTTT 417  
 Db 608 GTCTCTACCGGGCCCCAGAGGGGACACAGACGGGCTGTTTCGAGATGGCACTGGTG 667  
 Qy 418 TGGATACTGGCTTTCTTTGGTAAATGGCCCGATGATGATGATGATGATGATGATGATGAT 466





QY 958 CCATCTGCTGCTTCAATGCTCTTCACTTACCCAGAACGAGCCCAATCG 1017  
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 QY 1018 GTGTGGTACAGCATGCTCTGCTGCAATGCTTCAATGCTTGTAAATCCCTTCTG 1077  
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 Db 286 GTTCTCTATCAATTTACCTTTTGGCTTTTGTGATCAATCTCTCTGAAACCATTCCTC 345  
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 QY 1078 TACCCCTTGTGTACAGGCGTTTCCAGAGGCTTTCTGGAAGATACTTTGTGTGACAAA 1136  
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 Db 346 TACCCTCTCTGTCATGATAAATTCGAATGGCTTTTATGAAATATTTATGTCCTCCAGAA 404  
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RESULT 14  
 BU468854 754 bp mRNA linear EST 30-NOV-2002  
 LOCUS 603373878F1 CSEQRBN20 Gallus gallus cDNA clone CHEST284119 5', mRNA  
 DEFINITION sequence.  
 BU468854  
 ACCESSION BU468854.1 GI:25962431  
 VERSION EST.  
 KEYWORDS Gallus gallus (chicken)  
 SOURCE Gallus gallus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 754)  
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 22335534  
 12445392  
 CONTACT: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 1..754  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Laver and broiler"  
 /db\_xref="taxon:9031"  
 /clone="CHEST284119"  
 /sex="Male and female"  
 /tissue\_type="Chondrocytes isolated from growth plate  
 cartilage"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQRBN20"  
 /note="Vector: pBluescript II KS(+); Site 1: EcoRI;  
 Site 2: NotI; This normalized library was constructed from  
 1 million independent clones. cDNA synthesis was initiated  
 using an oligo(dT) primer, using methylated C in the first  
 strand synthesis reaction. Following this first strand  
 reaction, double-stranded cDNA was blunt-ended, ligated to  
 NotI adapters, digested with EcoRI, size-selected, and  
 cloned into the NotI and EcoRI compatible sites of a  
 custom modified MCS of the pBluescript (KS+) vector. The  
 library was normalized in 2 rounds using conditions  
 adapted from Soares et al., PNAS (1994) 91: 9228-9232 and  
 Bonaldo et al., Genome Research 6 (1996): 791, except that  
 a significantly longer reannealing hybridization was  
 used."

## ORIGIN

Query Match 6.9%; Score 80.6; DB 5; Length 754;  
 Best Local Similarity 61.5%; Pred. No. 4.5e-12;  
 Matches 147; Conservative 0; Mismatches 89; Indels 3; Gaps 1;

QY 898 GGCAGGAAGCTAGCCAGGTCACTGSCCATCTCTTCTGAGCGCTTTTGCCATTTGCTGGGCT 957  
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 Db 158 GACAAGAAGATTGCAAAAGTCACTTGCCATAATTTGTGTGCTTTTGCCATTTGCTGGGCC 217  
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 QY 958 CCATCTGCTGCTTCAATGCTCTTCACTTACCCAGAACGAGCCCAATCG 1017  
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 Db 218 CCATATACTTTAGTAATGAATTTATTCGTGGAGCGCTGCC---AAAGTGAATGTGTCCATTCA 274  
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 QY 1018 GTGTGGTACAGCATGCTCTGCTGCAATGCTTCAATGCTTGTAAATCCCTTCTG 1077  
 |||||  
 Db 275 GTTCTCTATCAATTTACCTTTTGGCTTTTGGATCAATTTCTCTGAAACCATTCCTC 334  
 |||||  
 QY 1078 TACCCCTTGTGTACAGGCGTTTCCAGAGGCTTTCTGGAAGATACTTTGTGTGACAAA 1136  
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 Db 335 TACCCTCTCTGTCATGATAAATTCGAATGGCTTTTATGAAATATTTATGTCCTCCAGAA 393  
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RESULT 15  
 BU468854 505 bp mRNA linear EST 09-JAN-2003  
 LOCUS rf37e04.v1 Meloidogyne hapla J2 pAMP1 v1 Meloidogyne hapla cDNA 5',  
 DEFINITION similar to TR:Q9XW31 Q9XW31 Y40H4A.1 PROTEIN. [1] ; mRNA sequence.  
 BU468854  
 ACCESSION BU468854.1 GI:22141376  
 VERSION EST.  
 KEYWORDS Meloidogyne hapla  
 SOURCE Meloidogyne hapla  
 ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
 Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.  
 1 (bases 1 to 505)  
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
 Willie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
 Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
 Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
 Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, I.,  
 Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
 McCann, R., Waterston, R. and Wilson, R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 CONTACT: McCarter, JP  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone will not be made available due to an unidentified  
 microbial contamination of the source material.  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 407.  
 Location/Qualifiers  
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 /dev\_stage="J2"  
 /lab\_host="DH10B"  
 /clone\_lib="Meloidogyne hapla J2 pAMP1 v1"  
 /note="vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;  
 The library was constructed by Claire Murphy and Dr. James  
 McCarter at Washington University, St. Louis. The cDNA was  
 made by using Dynabead oligo-dT priming (Dynal). PCR based  
 library using a modified protocol from the SMART PCR cDNA  
 Synthesis Kit from Clontech. Directionally cloned into the  
 UDG sites of pAMP1. J2 were provided by Dr. Valerie  
 Williamson of the University of California at Davis  
 (vmwilliamson@ucdavis.edu)."

## ORIGIN

Query Match 6.8%; Score 80.4; DB 5; Length 505;  
 Best Local Similarity 55.3%; Pred. No. 4.5e-12;  
 Matches 178; Conservative 0; Mismatches 141; Indels 3; Gaps 1;



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Qy 53 TGGCATTTTTAAGTCTTCATTGGCCCTTGGCTATATGGTAGGCAATGCTGTGTCATCT 112
Db 21 TTGTAATATTGGATTAATTTTCTCATTAGCTACAAGATCGGGAATGCTCTTGTATGC 80
Qy 113 TAGCCCTTTGGTGGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAAATTGG 172
Db 81 TTTCTATTTGTTGTTGATATAAAATTAACAACAATTAGCAATTAATTTCTTTCTTTAG 140
Qy 173 CTATTTCTGACTTCCTCGTGGGTTTGATTTCCATTCTC---TGTACATCCCTCAGTGT 229
Db 141 CTGTTGCTGATCTACTAATTTGGGCTTAATTTCTATCTCTTATGTTTCTATATACGCCAA 200
Qy 230 TGTTTAACTCGAAATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTACTGACTATCTTT 289
Db 201 ATGAGACTTGGACTTTTGGTTATCTCTTTGTCAATCTGGCTCTGTATAGATTATTAA 260
Qy 290 TGTGCACCGCATCTGTCTACAATATTGTCTCATTAGCTACGATCGATACCACTCAGTTT 349
Db 261 TGTGCAATGCTTCAGCACTCAATTTGTTATTAAATTAGCTTTGATAGATACTTTTCTGTTA 320
Qy 350 CAAATGCTGTGCTTATAGGCC 371
Db 321 CCCGACCTTTAACTTACAGGCC 342

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Search completed: April 7, 2005, 01:46:09  
Job time : 4431 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:36:06 ; Search time 90 Seconds  
(without alignments)  
1680.259 Million cell updates/sec

Title: US-10-626-445-8  
Perfect score: 2048  
Sequence: 1 MSENSTGILPPAAQVPLAF.....WKILCVTKRPALSONQSVSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2035	99.4	391	5	Aam50565 Mouse his
2	2035	99.4	391	8	Ado29497 Mouse GPC
3	1745	85.2	391	5	Aam50566 Rat hist
4	1370.5	66.9	390	3	Aab02831 Human G p
5	1370.5	66.9	390	3	Aay71297 Human orp
6	1370.5	66.9	390	4	Aab62445 Human GPC
7	1370.5	66.9	390	4	Aag64477 Human G p
8	1370.5	66.9	390	4	Aab73622 Human G p
9	1370.5	66.9	390	5	Aam53050 Human G p
10	1370.5	66.9	390	5	Abp98629 Human his
11	1370.5	66.9	390	5	Abp78276 Amino aci
12	1370.5	66.9	390	5	Aam50564 Human his
13	1370.5	66.9	390	5	Aag66023 Human his
14	1370.5	66.9	390	5	Aau74906 Amino aci
15	1370.5	66.9	390	6	Abg71960 Human G-p
16	1370.5	66.9	390	6	Abu92265 Human G p
17	1370.5	66.9	390	6	Abp81727 Human his
18	1370.5	66.9	390	6	Aae36417 Human H4
19	1370.5	66.9	390	7	Adg98760 Human orp
20	1370.5	66.9	390	7	Adj26923 Human end
21	1370.5	66.9	390	8	Adg86375 Human end
22	1370.5	66.9	390	8	Adj88376 Novel hum
23	1370.5	66.9	390	8	Ado05720 Human his
24	1370.5	66.9	390	8	Ado29496 Human GPC
25	1370.5	66.9	390	8	Adp20168 Human G p

26	1370.5	66.9	390	8	Adq75074 Human G p
27	1370.5	66.9	391	5	Aam53052 Human G p
28	1370.5	66.9	392	5	Aam53053 Human G p
29	1366.5	66.7	390	4	Aam51410 Human GPR
30	1366.5	66.7	390	6	Aae36416 Human H4
31	1365.5	66.7	390	8	Adg86522 Human end
32	1238	60.4	389	5	Aam50567 Guinea pi
33	1198	58.5	357	6	Aae36415 Human H4
34	1074.5	52.5	336	6	Aae36414 Human H4
35	729.5	35.6	415	7	Aao29530 Human H3
36	722.5	35.3	445	2	Aay92975 Human mac
37	722.5	35.3	445	2	Aay06322 Human G p
38	722.5	35.3	445	2	Aag67830 Human mus
39	722.5	35.3	445	3	Aay92218 Human his
40	722.5	35.3	445	4	Aab30627 A human h
41	722.5	35.3	445	5	Abb79792 Human his
42	722.5	35.3	445	6	AbR43667 Human his
43	722.5	35.3	445	6	Abp57425 Human his
44	722.5	35.3	445	6	Aao19746 Human his
45	722.5	35.3	445	6	Abp81687 Human his

## ALIGNMENTS

RESULT 1  
AAM50565  
ID AAM50565 standard; protein; 391 AA.  
XX  
AC AAM50565;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Mouse histamine H4 receptor.  
XX  
KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy.  
XX  
OS Mus musculus.  
XX  
PN WO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US005914.  
XX  
PR 31-MAY-2000; 2000US-0208260P.  
XX  
(ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
Lovenberg T, Liu C;  
XX  
WPI; 2002-114339/15.  
XX  
N-PSDB; AAI70981.  
XX  
New mammalian histamine H4 receptor proteins and polynucleotides encoding  
the proteins, useful in gene therapy for treating diseases where it is  
beneficial to elevate mammalian histamine H4 receptor activity.  
XX  
Claim 13; Fig 5B; 92pp; English.  
XX  
The present sequence is that of a mouse histamine receptor of the H4  
subtype, as predicted from a cDNA clone isolated from a spleen cDNA  
library. The invention provides mammalian (human, mouse, rat and guinea  
pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
recombinant host cells that produce active recombinant protein. The  
pharmacology of known histamine ligands is demonstrated. Mammalian  
histamine H4 receptor may be used in gene therapy for the treatment of  
diseases where it is beneficial to elevate mammalian histamine H4  
receptor activity. Recombinant protein is useful for identifying  
modulators of the histamine H4 receptor. Such modulators may be useful

CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
 CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
 CC the neuroendocrine system, stress and spasticity  
 XX  
 SQ Sequence 391 AA;  
 Query Match 99.4%; Score 2035; DB 5; Length 391;  
 Best Local Similarity 99.7%; Pred. No. 6.7e-202;  
 Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MSESNTGILPPAAQVPLAFMSSFAFAIMVGNVAVILAFVVDRLNLRHSNYFFLNLAIS 60  
 Db 1 MSESNTGILPPAAQVPLAFMSSFAFAIMVGNVAVILAFVVDRLNLRHSNYFFLNLAIS 60  
 QY 61 DFLVGLISPLTYPHVLFNNFGSGICMFWLIIDYLLCTASVYVNIIVLSYDRYQSVSNV 120  
 Db 61 DFLVGLISPLTYPHVLFNNFGSGICMFWLIIDYLLCTASVYVNIIVLSYDRYQSVSNV 120  
 QY 121 SYRAQHTGIMKIVAQVAVVILAFVNGPMLASDSWKNSNTNKDCEPGVTEWYILITIT 180  
 Db 121 SYRAQHTGIMKIVAQVAVVILAFVNGPMLASDSWKNSNTNKDCEPGVTEWYILITIT 180  
 QY 181 MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPESHAGFTSTSSASGHLHRAGVACRTSN 240  
 Db 181 MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPESHAGFTSTSSASGHLHRAGVACRTSN 240  
 QY 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGSEFWRSESAALRQRYAEILLRG 300  
 Db 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGSEFWRSESAALRQRYAEILLRG 300  
 QY 301 RKLARSAILLSAFACWAPYCLFTVLSYPTERPKSVVYSIAFWLQWNSFVNPELY 360  
 Db 301 RKLARSAILLSAFACWAPYCLFTVLSYPTERPKSVVYSIAFWLQWNSFVNPELY 360  
 QY 361 PLCHRRFQKAFWILCVTKQPALSQNSQSVSS 391  
 Db 361 PLCHRRFQKAFWILCVTKQPALSQNSQSVSS 391  
 RESULT 2  
 AD029497  
 ID AD029497 standard; protein; 391 AA.  
 XX  
 AC AD029497;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Mouse GPCR HRH4, SEQ ID NO:599.  
 XX  
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KW transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;  
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
 KW kidney disorder; liver disorder; lung disorder; breast disorder;  
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; antinemic;  
 KW cytostatic; antiinflammatory; vasotropic; antiangiinal; antiarrhythmic;  
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
 KW virocidic; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
 KW dermatological; antitumor; antichryoid; antiallergic; anorectic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
 murine; receptor.  
 XX  
 OS Mus musculus.  
 XX  
 PN W02004040000-A2.  
 XX  
 PD 13-MAY-2004.  
 XX  
 PF 09-SEP-2003; 2003WO-US028226.

XX  
 PR 09-SEP-2002; 2002US-0409303P.  
 PR 09-APR-2003; 2003US-0461329P.  
 XX  
 PA (PRIM-) PRIMAL INC.  
 XX  
 PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
 PI Madisen L, McIlwain KL, Pavlova MN, Vaassilatis D, Zeng H;  
 XX  
 DR WPI; 2004-390329/36.  
 DR N-PSDB; ADO30257.  
 XX  
 PT Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 XX  
 PS Claim 151; SEQ ID NO 599; 542pp; English.  
 XX  
 CC The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridize to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders (e.g., autoimmune disorders or  
 CC anaemia or leukaemia); immune disorders (e.g., osteoarthritis, rheumatoid  
 CC AIDS); bone and joint disorders (e.g., metabolic or nutritive disorders (e.g.,  
 CC arthritis, gout or osteoporosis); metabolic or nutritive deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the  
 CC invention. Note: The full sequence data for this patent did not form part  
 CC of the printed specification; those sequences not shown were obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 391 AA;  
 Query Match 99.4%; Score 2035; DB 8; Length 391;  
 Best Local Similarity 99.7%; Pred. No. 6.7e-202;  
 Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MSESNTGILPPAAQVPLAFMSSFAFAIMVGNVAVILAFVVDRLNLRHSNYFFLNLAIS 60  
 Db 1 MSESNTGILPPAAQVPLAFMSSFAFAIMVGNVAVILAFVVDRLNLRHSNYFFLNLAIS 60  
 QY 61 DFLVGLISPLTYPHVLFNNFGSGICMFWLIIDYLLCTASVYVNIIVLSYDRYQSVSNV 120  
 Db 61 DFLVGLISPLTYPHVLFNNFGSGICMFWLIIDYLLCTASVYVNIIVLSYDRYQSVSNV 120  
 QY 121 SYRAQHTGIMKIVAQVAVVILAFVNGPMLASDSWKNSNTNKDCEPGVTEWYILITIT 180  
 Db 121 SYRAQHTGIMKIVAQVAVVILAFVNGPMLASDSWKNSNTNKDCEPGVTEWYILITIT 180  
 QY 181 MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPESHAGFTSTSSASGHLHRAGVACRTSN 240  
 Db 181 MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPESHAGFTSTSSASGHLHRAGVACRTSN 240





Db 1 MPDNTNLSLSTRVTLAFNLSLVAFAIMLGNALVILAFVVDKRLHRSYFFFLNLAIS 60  
Qy 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVNAV 120  
Db 61 DFFGVGISIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYNIVLISYDRYQSVNAV 120  
Qy 121 SYRAQHTGIMKIVAQVAVWILAFVNGPMLASDKNSTNTKDCPEGFVTEWYILIT 180  
Db 121 SYRTQHTGVLKIVLWAVVWILAFVNGPMLVLSSESWKDEGS--ECEPGFSEWYILAIT 178  
Qy 181 MLEFLLPVISVAYENVVYINSLWKRRLSRCPHAGSTSSASGHLHAGVACRTSN 240  
Db 179 SFLEFVPIVILVAYFNMMIYNSLWKRDLHSLRCQSHPGLTAVSSNTCGHSFGRLSRRSL 238  
Qy 241 PGLKESAAHSRSESPRRKSSILVSLRTHMNSSITAFKVGSEFWRSESAALRORAEVALLRG 300  
Db 239 SASTEVPAFSEHSEQRKSSLMFSRTKNSNTIASKWGSQSDSVLHQHREHVELLRA 298  
Qy 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVMYSIAMWQFNFSFVNPLY 360  
Db 299 RRLAKSLAILLGVPACVWAPYSLFTIVLSFYSSATGPKSVWYRIAFWQFNFSFVNPLY 358  
Qy 361 PLCHRRFOKAFWKILCVTKWPAISO-NQSVSS 391  
Db 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 6  
AAB62445  
ID AAB62445 standard; protein; 390 AA.  
XX AC AAB62445;  
XX DT 09-JUL-2001 (first entry)  
XX DE Human GPCR-like polypeptide, PFI-013.  
XX KW G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;  
XX KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;  
XX KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;  
XX KW signal transduction.  
XX OS Homo sapiens.  
XX PN EP1096009-A1.  
XX PD 02-MAY-2001.  
XX PF 24-OCT-2000; 2000EP-00309364.  
XX PR 29-OCT-1999; 95GB-00025641.  
XX PR 20-APR-2000; 2000GB-00009973.  
XX PA (PFI2) PFIZER LTD.  
XX PA (PFI2) PFIZER INC.  
XX PI Peter B, O'reilly MA;  
XX DR WPI; 2001-309854/33.  
XX DR N-ESDB; AAF83203.  
XX PT New G-protein coupled receptor-like polypeptide, polynucleotide for  
XX PT screening drug candidates for treating diseases associated with signal  
XX PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.  
XX FS Claim 22; Page 44; 66pp; English.  
XX CC This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-  
XX CC 013, encoded by cDNA of NCIMB 41073. The PFI-013 protein can be expressed  
XX CC by standard recombinant methodology. Antibodies and modulators of PFI-013  
XX CC are useful in the manufacture of a medicament for treating allergic  
XX CC disorder, including extrinsic asthma, immunological disorders, such as

CC intrinsic asthma, vasculitic granulomatous disease, interstitial and  
CC other pulmonary disease, including chronic obstructive pulmonary disease  
CC (COPD), infectious, inflammatory disease, such as inflammatory bowel  
CC disease and neoplastic and myeloproliferative diseases. They are also  
CC useful for treating obesity, diabetes, metabolic, neurological diseases,  
CC psychotherapeutics, urogenital disease, reproduction and sexual medicine,  
CC inflammation, cancer, tissue repair, dermatology, photoaging, skin  
CC pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases,  
CC allergy and respiratory disease, sensory organ disorders, sleep disorders  
CC and hair loss. The PFI-013 protein and nucleic acid are useful in the  
CC diagnosis and treatment of the above conditions and also for screening  
CC drug candidates for the treatment of diseases associated with signal  
CC transduction. The antibodies are also useful for enrichment of  
CC eosinophils from mammalian, especially human blood and for detecting the  
CC protein in biological samples  
XX SQ Sequence 390 AA;  
Query Match 66.9%; Score 1370.5; DB 4; Length 390;  
Best Local Similarity 68.1%; Pred. No. 5.3e-133;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
Qy 1 MSESNTGILPPAAQVPLAFILMSSFAFIMVGNVILAFVVDKRLHRSYFFFLNLAIS 60  
Db 1 MPDNTNLSLSTRVTLAFNLSLVAFAIMLGNALVILAFVVDKRLHRSYFFFLNLAIS 60  
Qy 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVNAV 120  
Db 61 DFFGVGISIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYNIVLISYDRYQSVNAV 120  
Qy 121 SYRAQHTGIMKIVAQVAVWILAFVNGPMLASDKNSTNTKDCPEGFVTEWYILIT 180  
Db 121 SYRTQHTGVLKIVLWAVVWILAFVNGPMLVLSSESWKDEGS--ECEPGFSEWYILAIT 178  
Qy 181 MLEFLLPVISVAYENVVYINSLWKRRLSRCPHAGSTSSASGHLHAGVACRTSN 240  
Db 179 SFLEFVPIVILVAYFNMMIYNSLWKRDLHSLRCQSHPGLTAVSSNTCGHSFGRLSRRSL 238  
Qy 241 PGLKESAAHSRSESPRRKSSILVSLRTHMNSSITAFKVGSEFWRSESAALRORAEVALLRG 300  
Db 239 SASTEVPAFSEHSEQRKSSLMFSRTKNSNTIASKWGSQSDSVLHQHREHVELLRA 298  
Qy 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVMYSIAMWQFNFSFVNPLY 360  
Db 299 RRLAKSLAILLGVPACVWAPYSLFTIVLSFYSSATGPKSVWYRIAFWQFNFSFVNPLY 358  
Qy 361 PLCHRRFOKAFWKILCVTKWPAISO-NQSVSS 391  
Db 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRSVSS 390  
RESULT 7  
AAG64477  
ID AAG64477 standard; protein; 390 AA.  
XX AC AAG64477;  
XX DT 25-SEP-2001 (first entry)  
XX DE Human G protein-coupled receptor protein BG26.  
XX KW Human; G protein-coupled receptor protein BG26; histamine H3; histamine;  
XX KW altering intracellular cAMP concentration;  
XX KW regulating signal transduction.  
XX OS Homo sapiens.  
XX PN WO200146414-A1.  
XX PD 28-JUN-2001.  
XX PF 20-DEC-2000; 2000WO-JP009038.





[illegible]

Db 121 SYRTQHTGVLKIVTLMAVAVMLAFVNGPMLVSESWKDEGS--ECEPGFFSEWYLAIT 178

Qy 181 MLEFLLPVISVAYENVQIYWSLWKRRLSCPSHAGFTTSSASGHLHRAGVACRTSN 240

Db 179 SFLEFVPIVILVAYFNKNIYWSLWKRDLHLSRCOSHPLGTAVSNNICGHSGFRGLSRRSL 238

Qy 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSSTITAFKVGSMFVSESAALRQREYAEALLRG 300

Db 239 SASTEVPAFHSERQRRKSSLMFSSRTKNSNTIASKMGFSQSDSVALHQREHVELLRA 298

Qy 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPFY 360

Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFY 358

Qy 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391

Db 359 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 390

RESULT 10

ABP98629

ID ABP98629 standard; protein; 390 AA.

XX

AC ABP98629;

DT 13-JUN-2003 (first entry)

XX

DE Human histamine receptor SP9144.

XX

XX human; histamine receptor; chromosome 18; anti-inflammatory;

KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;

KW anti-migraine; cardiast; anti-rheumatic; anti-arthritis; antipsoriatic;

KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;

KW myocardial infarction; migraine; chronic obstructive pulmonary disease;

KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;

KW psoriasis; receptor.

XX

OS Homo sapiens.

XX

PN US6204017-B1.

XX

PD 20-MAR-2001.

XX

PF 07-OCT-1999; 99US-00414010.

XX

XX 07-OCT-1999; 99US-00414010.

PR (SCHE ) SCHERING CORP.

XX

PA Behan JX, Hedrick JA, Laz TM, Monema FJ, Morse KL, Umland SP;

PI Wang S;

XX

XX WPI; 2002-442063/47.

DR N-PSDB; ABZ80663.

XX

XX New nucleic acid encoding antigenic part of human histamine receptor,

PT useful for preparing antibodies, e.g. for treating-histamine related

PT disorders.

XX

PS Example 1; Col 27-30; 19pp; English.

XX

XX This sequence represents the amino acid sequence of a human histamine

CC receptor (HR) designated SP9144. The sequence was isolated by searching

CC databases with the sequence of known G-coupled protein receptor (GPCR).

CC The gene is used for recombinant production of HR and for preparing

CC antibodies (Ab). These Ab are used to purify HR by immunoaffinity

CC chromatography, in immunosay of histamine receptor, to identify cDNA

CC clones that express the receptor, as antagonist to block binding of

CC histamine (for treating any histamine-associated disorder) and to

CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR

CC protein can be used in the treatment of e.g. inflammation, asthma,

CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,

CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple

CC sclerosis, inflammatory bowel disease and psoriasis

XX

SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 5; Length 390;

Best Local Similarity 68.1%; Pred. NO. 5.3e-133;

Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy 1 MSESNTGLPPAAQVPLAFLMSFAFAIMVGNVAVILAFVVDNRNLRHSNYFFLNLAIS 60

Db 1 MPDNTSTINLSUSTRVTLAFLMSVAFATMLGNALVILAFVVDNRNLRHSNYFFLNLAIS 60

Qy 61 DFLVGLISIPLYIPHLFNNRFGSGICMEWLITDYLLCTASVYVNIIVLISYDRYQSVNAV 120

Db 61 DFLVGLISIPLYIPHLFNNRFGSGICMEWLITDYLLCTASVYVNIIVLISYDRYQSVNAV 120

Qy 121 SYRAQHTGIMKIQAQMVAVMILAFVNGPMLIASWKNSTNTKDCPEPGFVTEWYLAIT 180

Db 121 SYRTQHTGVLKIVTLMAVAVMLAFVNGPMLVSESWKDEGS--ECEPGFFSEWYLAIT 178

Qy 181 MLEFLLPVISVAYENVQIYWSLWKRRLSCPSHAGFTTSSASGHLHRAGVACRTSN 240

Db 179 SFLEFVPIVILVAYFNKNIYWSLWKRDLHLSRCOSHPLGTAVSNNICGHSGFRGLSRRSL 238

Qy 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSSTITAFKVGSMFVSESAALRQREYAEALLRG 300

Db 239 SASTEVPAFHSERQRRKSSLMFSSRTKNSNTIASKMGFSQSDSVALHQREHVELLRA 298

Qy 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPFY 360

Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFY 358

Qy 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391

Db 359 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 390

RESULT 11

ABB78276

ID ABB78276 standard; protein; 390 AA.

XX

AC ABB78276;

DT 05-DEC-2002 (first entry)

XX

DE Amino acid sequence of human histamine receptor.

XX

KW Human; histamine receptor; receptor; inflammation; asthma; allergy;

KW atopic dermatitis; stroke; myocardial infection; migraine;

KW chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;

KW multiple sclerosis; inflammatory bowel disease; psoriasis;

KW intracellular second messenger pathway; cellular growth rate;

KW hormone secretion.

XX

OS Homo sapiens.

XX

PN US2002098539-A1.

XX

PD 25-JUL-2002.

XX

PF 19-MAR-2001; 2001US-00812216.

XX

XX 07-OCT-1999; 99US-00414010.

PR (BEHA/) BEHAN J X.

PA (HEDR/) HEDRICK J A.

PA (LAZT/) LAZ T M.

PA (MONS/) MONSMA F J.

PA (MORS/) MORSE K L.

PA (UMLA/) UMLAND S P.

PA (WANG/) WANG S.

XX

PI Behan JX, Hedrick JA, Laz TM, Monema FJ, Morse KL, Umland SP;

PI Wang S;  
 XX WPI; 2002-673827/72.  
 DR N-PSDB; ABW78739.  
 XX  
 XX Novel mammalian histamine receptor polypeptide useful for identifying  
 PT agonist or antagonist for treating diseases such as inflammation, asthma,  
 PT stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.  
 XX  
 PS Claim 2; Page 16-17; 21pp; English.  
 XX  
 CC The present sequence represents a histamine receptor. The polypeptide is  
 CC useful for identifying an agonist or antagonist of a mammalian histamine  
 CC receptor. It is useful as an antigen to elicit the production of  
 CC antibodies. The histamine receptor polypeptide and polynucleotide are  
 CC useful in the treatment and management of diseases such as inflammation,  
 CC asthma, allergy, atopic dermatitis, stroke, myocardial infection,  
 CC migraine, chronic obstructive pulmonary disease (COPD), rheumatoid  
 CC arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.  
 CC They are also useful for modulating intracellular second messenger  
 CC pathway activated through histamine receptors (cyclic-AMP, calcium,  
 CC inositol phosphate and mitogen activated protein (MAP) kinase), changes  
 CC in cellular growth rate, secretion of hormones, receptor-stimulated Ca<sup>2+</sup>  
 CC mobilization, mitogenic effects, etc  
 XX  
 SQ Sequence 390 AA;  
 Query Match 66.9%; Score 1370.5; DB 5; Length 390;  
 Best Local Similarity 68.1%; Pred. No. 5.3e-133;  
 Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
 Qy 1 MSENSTGILPPAAQVPLAFMLSSFAFAMVGNVAVILAFVVDRLHRSNYFFLNLAIS 60  
 Db 1 MPDNTNINLSLSTRTVLAPFMSLVAFALMLGNALVILAFVVDKRLHRSYFFLNLAIS 60  
 Qy 61 DFLVGLISIPLYIPIHVLNFWNFGSGICMFMLTDYLLCTASVYVILISYDRYQSVNAV 120  
 Db 61 DFFVGVISIPLYIPIHTLFEWDFGKEICVFWLTDYLLCTASVYVILISYDRYQSVNAV 120  
 Qy 121 SYRQHTGVLKIVLWVAVVWVLAFLVNGPMLVSDSKNSTNTKDCPFGFVTEWYILTIT 180  
 Db 121 SYRQHTGVLKIVLWVAVVWVLAFLVNGPMLVSDSKNSTNTKDCPFGFSEWYILAIT 178  
 Qy 181 MLLEFLPLVSVAYFNVQIYWSLWKRRLSRCPHAGFTTSSASGHLHAGVACRTSN 240  
 Db 179 SFLEFVPIVLVAYFNNIYWSLWKRDLHRCQSHPGTLAVSSNICGHSFGRSSRL 238  
 Qy 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGFWRSAAALRQREVAELRG 300  
 Db 239 SASTEVPAFSPHSEQRKSSLMFSSRTYKMSNTTASKMGFSQSDSVLHQREHVELLRA 298  
 Qy 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPLY 360  
 Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYRIAFAFWLQWFNSFVNPLY 358  
 Qy 361 PLCHRRFQKAFWKILCVTKWPAALSQ-NQSVSS 391  
 Db 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRSVSS 390  
 RESULT 12  
 AAM50564  
 ID AAM50564 standard; protein; 390 AA.  
 XX  
 AC AAM50564;  
 XX  
 DT 18-MAR-2002 (first entry)  
 XX  
 DE Human histamine H4 receptor.  
 KW Histamine H4 receptor; human; antiasthmatic; antiallergenic;  
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
 KW diagnosis; gene therapy.

XX Homo sapiens.  
 OS WO200192485-A1.  
 PN  
 XX  
 PD 06-DEC-2001.  
 XX  
 XX 22-FEB-2001; 2001WO-US005914.  
 PF  
 XX 31-MAY-2000; 2000US-0208260P.  
 PR  
 XX (ORTH ) ORTHO-MCNEIL PHARM INC.  
 PA  
 XX Lovenberg T, Liu C;  
 FI  
 XX WPI; 2002-114339/15.  
 XX N-PSDB; AAI70980.  
 DR  
 XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX  
 PS Claim 13; Fig 2; 92pp; English.  
 XX  
 CC The present sequence is that of a human histamine receptor of the H4  
 CC subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA  
 CC library. The invention provides mammalian (human, mouse, rat and guinea  
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
 CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the human histamine H4 receptor. Such modulators may be  
 CC useful for diagnosing, creating or preventing asthma, allergy,  
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity  
 XX  
 SQ Sequence 390 AA;  
 Query Match 66.9%; Score 1370.5; DB 5; Length 390;  
 Best Local Similarity 68.1%; Pred. No. 5.3e-133;  
 Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
 Qy 1 MSENSTGILPPAAQVPLAFMLSSFAFAMVGNVAVILAFVVDRLHRSNYFFLNLAIS 60  
 Db 1 MPDNTNINLSLSTRTVLAPFMSLVAFALMLGNALVILAFVVDKRLHRSYFFLNLAIS 60  
 Qy 61 DFLVGLISIPLYIPIHVLNFWNFGSGICMFMLTDYLLCTASVYVILISYDRYQSVNAV 120  
 Db 61 DFFVGVISIPLYIPIHTLFEWDFGKEICVFWLTDYLLCTASVYVILISYDRYQSVNAV 120  
 Qy 121 SYRQHTGVLKIVLWVAVVWVLAFLVNGPMLVSDSKNSTNTKDCPFGFVTEWYILTIT 180  
 Db 121 SYRQHTGVLKIVLWVAVVWVLAFLVNGPMLVSDSKNSTNTKDCPFGFSEWYILAIT 178  
 Qy 181 MLLEFLPLVSVAYFNVQIYWSLWKRRLSRCPHAGFTTSSASGHLHAGVACRTSN 240  
 Db 179 SFLEFVPIVLVAYFNNIYWSLWKRDLHRCQSHPGTLAVSSNICGHSFGRSSRL 238  
 Qy 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGFWRSAAALRQREVAELRG 300  
 Db 239 SASTEVPAFSPHSEQRKSSLMFSSRTYKMSNTTASKMGFSQSDSVLHQREHVELLRA 298  
 Qy 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPLY 360  
 Db 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYRIAFAFWLQWFNSFVNPLY 358  
 Qy 361 PLCHRRFQKAFWKILCVTKWPAALSQ-NQSVSS 391  
 Db 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRSVSS 390



modulators of signal transduction for treating kidney disease, hyperlipidemia, obesity, dyslexia and cardiac myxoma.

Claim 26; Page 61; 78pp; English.

The present invention relates to a new G-protein coupled receptor (GPCR) polypeptide comprising greater than 70% amino acid sequence identity to the amino acid sequence of human GPCR62, TGR21, TGR130.1, TGR130.2, human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18 or 90% amino acid sequence identity to human novel edg receptor protein, as defined in the specification. The GPCR covalently linked to a solid phase is useful for identifying a compound that modulates signal transduction. The identified compounds are useful for treating kidney disease, cerebral cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac myxoma. The molecules of the invention are useful for diagnosing disorders or conditions such as kidney-related conditions or diseases such as renal failure, nephritis, nephrotic syndrome, asymptomatic urinary abnormalities, renal tubule defects, hypertension and nephrolithiasis, liver-related disease or condition e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice and spleen-associated disorders or conditions e.g. splenic enlargement, immune disorders, blood disorders and others. Modulation of the polypeptide of the invention is useful to treat or prevent any of the above conditions or diseases. The present amino acid sequence represents the human GPCR TGR62 protein of the invention. This sequence is one of seven novel G protein coupled receptors of the invention (AAU74904 - AAU74911).

	Matches	267;	Conservative	40;	Mismatches	82;	Indels	3;	Gaps	2;
Qy	1	MSEGNSTGILPAAQVLAFLWSSFAFAMVGNVAWILAFLVVDRNLRRHSNYFFLNLAIS	60	: : : : :	:	:	:	:	:	:
Dd	1	MPDTNSTINLSLSTRVLAFPMGLVAFIMUGNALVILAFVVDKDLRHRSSYFFLNLAIS	60	: : : : :	:	:	:	:	:	:
Qy	61	DFLVGLSIPLYIPHVLFNMMFGSGICWFMLITDYLCTASVYNIVILSYDRYOSVSNAV	120	: : : : :	:	:	:	:	:	:
Dd	61	DFFGVGVISIPLYIPIHTLFWDGFGEIKCVFWLTIDYLCTASVYNIVILSYDRYLSVNNAV	120	: : : : :	:	:	:	:	:	:
Qy	121	SYRAQTGIMKIQAQMAVAVILAFVLNGPMLIASDSWKNSNTNTKDCBPGFVTEWYILIT	180	: : : : :	:	:	:	:	:	:
Dd	121	SYRTQHTGVLIKVTLMVAVWLAFVLNGPMLIVSESWMKBEGS--ECBPGFPSEWYILAIT	178	: : : : :	:	:	:	:	:	:
Qy	181	MLEBFLLPVISVAYENVQIYWSLMKRLALSRCPSHAGFTSTTSSASGHHLRAGVACRTSN	240	: : : : :	:	:	:	:	:	:
Dd	179	SFLEFVIPVLVAYFNMMIYWSLWKDHLRSQCSPHGLTAVSSNICGHSFGRLLSSRSL	238	: : : : :	:	:	:	:	:	:
Qy	241	PGLKESAAARSHSESPRKSSILSVLRTHMNSSITAFKVGSPWRSESAAALROREYAELLRG	300	: : : : :	:	:	:	:	:	:
Dd	239	SASTEVPAAPHSERQRKRKSSLMFSSRTTKMSNTIAASKMGSPSQSDSVALLHQREHVELLRA	298	: : : : :	:	:	:	:	:	:
Qy	301	RKLARSLAILLSAPAIWAPLYCLTIIVLSTPYRTERPKSWYYSATFMLQWNFSFWNPFLY	360	: : : : :	:	:	:	:	:	:
Dd	299	RRLAKSLAILLGPAVCWAPYSLETIVLSFYSSATGPKSVMYRTAFMLQWNFSFWNPFLY	358	: : : : :	:	:	:	:	:	:
Qy	361	PLCHRRQKAFWKILCVTKWPALSQ-NQSUS	391	: : : : :	:	:	:	:	:	:
Dd	359	PLCHKRFQAFELKIFCIKKQLPPQHGRSVSS	390	: : : : :	:	:	:	:	:	:

Search completed: April 6, 2005, 19:31:30  
Job time : 97 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 19:10:42 ; Search time 27 Seconds  
(without alignments)  
1081.029 Million cell updates/sec

Title: US-10-626-445-8  
Perfect score: 2048  
Sequence: 1 MSENSTGILPPAAQVPLAF.....WKILCVTKWPALSNQSVSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1370.5	66.9	390	3	US-09-414-010-2
2	1370.5	66.9	390	4	US-09-812-216-2
3	722.5	35.3	445	2	US-08-985-090-2
4	722.5	35.3	445	3	US-09-165-543-2
5	722.5	35.3	445	3	US-09-167-354-7
6	722.5	35.3	445	4	US-09-642-855-7
7	722.5	35.3	445	4	US-09-642-514-7
8	722.5	35.3	449	4	US-09-949-016-10930
9	722.5	35.3	453	4	US-09-891-053-20
10	716.5	35.0	445	3	US-09-165-543-5
11	716.5	35.0	445	4	US-09-891-053-25
12	709.5	34.6	413	4	US-09-891-053-1
13	621.5	20.3	351	3	US-09-524-182-2
14	582.5	28.4	362	2	US-08-985-090-5
15	582.5	28.4	362	3	US-09-165-543-32
16	427	20.8	348	1	US-08-118-270-13
17	427	20.8	348	5	PCT-US93-08528-13
18	427	20.8	355	1	US-08-118-270-11
19	427	20.8	355	5	PCT-US93-08528-11
20	415.5	20.3	479	1	US-08-313-553-7
21	415.5	20.3	479	3	US-08-767-993-7
22	408	19.9	460	4	US-09-538-092-513
23	402.5	19.7	590	4	US-09-538-092-967
24	399.5	19.5	532	4	US-09-826-509-521
25	397.5	19.4	590	4	US-09-826-509-517
26	393	19.2	354	1	US-08-313-553-9
27	393	19.2	354	3	US-08-767-993-9

28	390.5	19.1	501	1	US-08-722-001-14	Sequence 14, Appl
29	390.5	19.1	501	2	US-08-467-568-9	Sequence 9, Appl
30	390.5	19.1	501	2	US-09-030-582-9	Sequence 9, Appl
31	389.5	19.0	513	3	US-08-406-855A-21	Sequence 21, Appl
32	389.5	19.0	513	3	US-09-206-899-21	Sequence 21, Appl
33	389.5	19.0	515	1	US-08-444-734A-7	Sequence 7, Appl
34	389.5	19.0	515	3	US-08-406-855A-22	Sequence 22, Appl
35	389.5	19.0	515	3	US-09-206-899-22	Sequence 22, Appl
36	388.5	19.0	400	4	US-09-826-509-491	Sequence 491, App
37	388.5	19.0	572	1	US-08-334-698-2	Sequence 2, Appl
38	388.5	19.0	572	1	US-08-228-932-2	Sequence 2, Appl
39	388.5	19.0	572	1	US-08-468-939-2	Sequence 2, Appl
40	388.5	19.0	572	1	US-08-722-001-30	Sequence 30, Appl
41	388.5	19.0	572	2	US-08-406-855A-2	Sequence 2, Appl
42	388.5	19.0	572	2	US-08-722-190-2	Sequence 2, Appl
43	388.5	19.0	572	3	US-08-244-354-2	Sequence 2, Appl
44	388.5	19.0	572	3	US-09-206-899-2	Sequence 2, Appl
45	388.5	19.0	572	4	US-09-444-783-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-414-010-2  
; Sequence 2, Application US/09414010  
; Patent No. 6204017  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monama, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/414.010  
; CURRENT FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-414-010-2

Query Match	66.9%	Score	1370.5	DB	3	Length	390
Best Local Similarity	68.1%	Pred. No.	8e-106				
Mismatches	267	Conservative	40	Mismatches	82	Indels	3
Gaps	2						
Qy	1	MSENSTGILPPAAQVPLAFILMSSFAFAMVGNNAVILAFVVDNRNLHRSNYEFLNLAI	60				
Db	1	MPDNTNINSLSRVTLAFMSLVAFAMIGNALVILAFVVDNRNLHRSNYEFLNLAI	60				
Qy	61	DFLVGLISIPYIPHLFNMNFGSGICFMWLTIDYLLCTASVYVNLISIDRYOSVSNV	120				
Db	61	DFFGVLSIPYIPHTLFWDGKEICVFWLTIDYLLCTASVYVNLISIDRYLSVSNV	120				
Qy	121	SYRAQHTGIMKIVAQMVAVILAFVNGPMILADSNNSTNTKDCBPGFVTEWILIT	180				
Db	121	SYRQHTGVLKIVLMVAVVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWILIT	178				
Qy	181	MLLEFLPVISVAVPNVQIYMSLWKRALSRCPSHAGFTSTSSASGHLHAGVACRTSN	240				
Db	179	SFLEFVPIVLVAVFNMNIYMSLWKRLSRCPHAGFTSTSSASGHLHAGVACRTSN	238				
Qy	241	PGLKESAAHRSSEPRKSSITLSLRTHMNSSITAFKVGFSFWRSESALRORVLAELRG	300				
Db	239	SASTEVPAFSEQRKRSLSIMFSSRTYMSNTTASKMGFSQSDSVLHOREHVELLRA	298				
Qy	301	RKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFMLOWFNPNPLY	360				



Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSPYSSATGPKSVWYRIAFWLQWNSFVNPLLY 358

Qy 361 PLCHRRFQKAFWKILCVTKWKPALSO-NQSVSS 391

Db 359 PLCHRRFQKAFWKILCVTKWKPALSO-NQSVSS 390

RESULT 2

US-09-812-216-2

Sequence 2, Application US/09812216

Patent No. 6613533

GENERAL INFORMATION:

APPLICANT: Behan, Jiang Xu

APPLICANT: Hedrick, Joseph A.

APPLICANT: Laz, Thomas M.

APPLICANT: Monema, Frederick J. Jr.

APPLICANT: Morse, Kelley L.

APPLICANT: Unland, Shelby P.

APPLICANT: Wang, Suke

TITLE OF INVENTION: Histamine receptor

FILE REFERENCES: CN01069

CURRENT APPLICATION NUMBER: US/09/812,216

CURRENT FILING DATE: 2001-03-19

PRIOR APPLICATION NUMBER: 09/414,010

PRIOR FILING DATE: 1999-10-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 390

TYPE: PRT

ORGANISM: Homo sapiens

US-09-812-216-2

Query Match 66.9%; Score 1370.5; DB 4; Length 390;

Best Local Similarity 68.1%; Pred. No. 8e-106;

Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy 1 MSESNTGILPPAAQVPLAFMSSFAFMVGNVILAFVVDNRNLRHSNFFFLNLAIS 60

Db 1 MPDNTNINLSLSTRTVTLAFMSSVAFIMLGNALVILAFVVDNRNLRHSNFFFLNLAIS 60

Qy 61 DFLVGLISIPLYIPIHVLNFGSGICMFWLITDYLLCTASVYNIIVLSYDRYQSVSNV 120

Db 61 DFLVGLISIPLYIPIHVLNFGSGICMFWLITDYLLCTASVYNIIVLSYDRYQSVSNV 120

Qy 121 SYRAQHTGIMKIVQAVMVLAFVGNVILAFVVDNRNLRHSNFFFLNLAIS 180

Db 121 SYRAQHTGIMKIVQAVMVLAFVGNVILAFVVDNRNLRHSNFFFLNLAIS 180

Qy 181 MLLEFLLPVISVAFVNVQIYVWLSLWKRRLSRCPHAGFTSSASGHLHRAGVACRTSN 240

Db 179 SFLEFVIVPLVAFVNVQIYVWLSLWKRDLHRSRCPHAGFTSSASGHLHRAGVACRTSN 238

Qy 241 PGLKESAAHSRSPRRKSSILVLRTHMNSSITAFKVSFWSESAAALRQRYAELLRG 300

Db 239 SASTEPASPHSRQRKSSLMFSRTKMSNTIASKGSFQSDSVLHQHVELLRA 298

Qy 301 RLKARSLAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYRIAFWLQWNSFVNPLLY 360

Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSPYSSATGPKSVWYRIAFWLQWNSFVNPLLY 358

Qy 361 PLCHRRFQKAFWKILCVTKWKPALSO-NQSVSS 391

Db 359 PLCHRRFQKAFWKILCVTKWKPALSO-NQSVSS 390

RESULT 3

US-08-985-090-2

Sequence 2, Application US/08985090

Patent No. 5885893

GENERAL INFORMATION:

APPLICANT: Andrew D.J. Goodearl

TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/985,090

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jean M. Silveri

REGISTRATION NUMBER: 39,030

REFERENCE/DOCKET NUMBER: MNI-032

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214, 2

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 445 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-985-090-2

Query Match 35.3%; Score 722.5; DB 2; Length 445;

Best Local Similarity 38.8%; Pred. No. 4.9e-52;

Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

Qy 18 LAFLMSSFAFMVGNVILAFVVDNRNLRHSNFFFLNLAISDFLVGLISIPLYIPIHVL 77

Db 37 LAALMALLIVATVLGNALVLAFAVDSSLRQNNFFLNLAISDFLVGLISIPLYIPIHVL 96

Qy 78 F-NMFGSGICMFWLITDYLLCTASVYNIIVLSYDRYQSVSNVSRQAHTGIMKIVQAV 136

Db 97 TGRWTFGRGLKMLVVDYLLCTSSAFNIVLSYDRFLSVTRAVSRAQGDTRRAVRKM 156

Qy 137 VAVWILAFVGNVILAFVVDNRNLRHSNFFFLNLAISDFLVGLISIPLYIPIHVL 191

Db 157 LLVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS 213

Qy 192 VAYFNVQIY-----WSLWKRRLSRCPH 215

Db 214 VTFFNLISYLNTRRLDLGAREAAAGPEPPPEAQSPPPPGCWGCWQKHGEAMPLH 273

Qy 216 -----AGFTTSSSSAGHLHRAGVACRTSNPGLKESAAHSRSPRRKSSILV 263

Db 274 RYGVGEAAVGAAGEATLGGGGG---GSVAIPSSSSG-----SSRGTGERPR----- 318

Qy 264 SLRTHMNSSITAFKVSFWSESAAALRQRYAELLRGKRLARSILLSAF 314

Db 319 -----SLKRGSKPSASSASLEKEMKMSQSFQRPRLSRDRKVAKSLAVIVSIF 367

Qy 315 AICWAPYCLFTIVLSTYPTERPKSVWYRIAFWLQWNSFVNPLLYPLCHRRFQKAFWKI 374

Db 368 GLCWAPYTLIMIRAAACHGHCVP-DYWYBTSFWLLMANSVAVNPVLYPLCHHFRFRAFTKL 426

Qy 375 LCVTK 379

Db 427 LCPQK 431

RESULT 4

US-09-165-543-2

```

: Sequence 2, Application US/09165543
: Patent No. 6093545
: GENERAL INFORMATION:
: APPLICANT: Andrew D. J. Goodearl and Sandra Glucksmann
: TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
: NUMBER OF SEQUENCES: 39
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD, LLP
: STREET: 28 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/165,543
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/042,780
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Elizabeth A. Hanley
: REGISTRATION NUMBER: 33,505
: REFERENCE/DOCKET NUMBER: MNI-032CP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)742-4214
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 445 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-165-543-2

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Query Match	35.3%	Score	722.5	DB	3	Length	445
Best Local Similarity	38.8%	Pred. No.	4.9e-52				
Matches	165	Conservative	51	Mismatches	116	Indels	93
						Gaps	10
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DB	37	LAALMALLIVATVUGNAUVMUAFVADSSLRQTQNNFFLLNLAISDFLVGAFCPIYIPVPL	96				
QY	78	F-NNFSGIGCMFWLITDYLLCTASVYNIIVLISYDRQSVSNVASYRAQHTGIMKIQAQM	136				
DB	97	TGRWTFGRGLCKLWVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAAQOQDTRRAVRKM	156				
QY	137	VAVWILAFVNGPMILASDSWK-----NSTWTKDCEPGFVTEWYILITITMLLEFLPVS	191				
DB	157	LLVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNNWYFLITASTLEFPTPLS	213				
QY	192	VAYFNVQIY-----WSLWKERALSRCPSH	215				
DB	214	VTFFNLISYLNIRQRTLRLDGAEEAGPEPPEAQSPPPPCWGCWQKGHEAMPLH	273				
QY	216	-----AGFSTTSSASGHLNRAGVACHTSNPLKESAAASHSESPPRKSSILV	263				
DB	274	RYGVGEAAVGAEEATLGGGGG-----GSVASPTSSG-----SSSRGTERPR	318				
QY	264	SLRTHMNSITAFKVFWSSESALRQR-----EYAEILLRGRKLARSLLAILSAF	314				
DB	319	-----SLKRGSKPSASSASLEKRMKMSVQSFTQRFSLSRDRKVAKSLAVISIF	367				
QY	315	AICWAPYCLTIVLSTYPRTERPKSVYVYSTAFNLQWFNSFVNPFLYPLCHRRPFOKATWKI	374				
DB	368	GLCWAPYTLMIIRAACHGHCVP-DYWYETSFWLLMWANSANVPVLYPLCHHSFFRAFTKL	426				
QY	375	LCVTK	379				

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Db      427 LCPQK 431
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RESULT 5
US-09-167-354-7
; Sequence 7, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JWV
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
; US-09-167-354-7

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Query Match	35.3%	Score	722.5	DB	3	Length	445
Best Local Similarity	38.8%	Pred. No.	4.9e-52				
Matches	165	Conservative	51	Mismatches	116	Indels	93
							Gaps 10
Qy	18	LAFIMSPFAIMVGNVAVLAFVDBNLRHSNYPFLNLAISDFVLGLAISPIXYIPVL	77				
Db	37	LAALMALLIVATVLGNALVMAFVADSLRQTNNFFLLNLAISDFLVGAFCIPLYPYVL	96				
Qy	78	F-NNFGSGICMFMLITDYLLCTASVNVILISVDRYQSVSNVSYRAOHTGIMKIYAQM	136				
Db	97	TGRWTFGRGLUCKLWVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRM	156				
Qy	137	VAVMILAFVLVNGPMILASDSWK-----NSTNTKDCEPGFVTEWYILITIMLLEFLLPVIS	191				
Db	157	LLVWVLAFLYGPAIL---SWEVLSCGSSIPPEGHCYAEFFFNWYFLITASTLEFFTPLS	213				
Qy	192	VAYVNVQIY-----WSLKKRRALSRCPSH	215				
Db	214	VTFFNLISYLNIRQRTLRRLDGLAREAAAGPEPPPEAQSPSPPPPCGCGWKGHGEAMPLH	273				
Qy	216	-----AGFSTTSSASGHLHRACVACTSNPGLKESANASHSSPRKSSILV	263				
Db	274	RYGVGEAAVGAEGATELGGGGG---GSVASPTSSG---SSSRGTERRP-----	318				
Qy	264	SLRTHNSSITAPKVSFWSESAALRQ-----EYAEILLRGLKARSILAILLSAF	314				
Db	319	-----SLRGSKPSASSASLEKRWKQVVSQFTQFRLSRDRKVAKSLAVISIF	367				
Qy	315	AICWAPCYLFTIVLSTYPRTERPKVSMYSIAFWLQMFNSFVNPFYPLCHRRRFQAFWKI	374				
Db	368	GLCWAPYLLMIIRAACHGHCVP-DYWYETSFWLLMANSANVPVLYPLCHHSFPRAFTKL	426				
Qy	375	LCVTK	379				
Db	427	LCPOK	431				

RESULT 6  
US-09-642-855-7  
: Sequence 7, Application US/09642855  
: Patent No. 6413743  
: GENERAL INFORMATION:  
: APPLICANT: Lovenberg, Timothy  
: APPLICANT: Erlander, Mark  
: APPLICANT: Pvari, Javashree  
: APPLICANT: Javashree

```

: Sequence 2, Application US/09165543
: Patent No. 6093545
: GENERAL INFORMATION:
: APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
: TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
: NUMBER OF SEQUENCES: 39
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD, LLP
: STREET: 28 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/165,543
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/042,780
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Elizabeth A. Hanley
: REGISTRATION NUMBER: 33,505
: REFERENCE/DOCKET NUMBER: MNI-032CP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)742-4214
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 445 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-165-543-2

Query Match 35.3%; Score 722.5; DB 3; Length 445;
Best Local Similarity 38.8%; Pred. No. 4.9e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 101

QY 18 LAFIMSSFAFPAIMGVNAWVILAFVVDVDRNLHRNSVFFLNLAISDFVLGLISPIYIPVL 77
Db 37 LAALMALLIVATVLCNALVMAFVADSSLRQNNFFLNLAISDFLVGAFICPIYXPVL 96

QY 78 F-NNFSGIGCMFLITDYLLCTASVYVNLISYDRYQSVSNVSYRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWVLDYLLCTSSAFNVILISYDRFLSVTVRAVSYRAQGDTRRAVRKM 156

QY 137 VAVWILAFVNGPMILASDHWK-----NSTNTKDCPGFTWETWILITMLLEFLLPVIS 191
Db 157 LLVWVLAFLLYGPAIL---SWEYILSGGSSIPEGHCYAEFFYNNYFLITASTLEFPTPLS 213

QY 192 VAFVNVQIY-----WSLWKRRALSRCPSH 215
Db 214. VTFNLISYLNIRQTRLRLDGAAREAGPEPPPEAQSPPPPPCGWCGWGHGEAMPLH 273

QY 216 -----AGFTSTSSASGHLHRAGVACRTSNPGLKESAAARHSESPPRKSITLV 263
Db 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG---SSSRGTERPR----- 318

QY 264 SLRTHNMSITAFKVGFWSESAAALRQ-----EYALLRGRKLARSAILLSAP 314
Db 319 -----SLKRGSKPSASSASLEKRMKWVSQSFTQRFLSRDRKRVAKSLAVISIF 367

QY 315 AICWAPYCLFTIVLSTYPRTERPKSVVSYAFMLQWENSFVNPFLYPLCHRRFQKAFWKI 374
Db 360 GLCWAPYTLMLIRAAACHGCVP--DYWTYETSFWLLWANSANPVLVPLCHHSFRFAFTKL 426

QY 375 LCVTK 379

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QY 231 RAGVACRTSNPGLKESASRHSERPRKSSILVSLRTHMNSSITAFKVGFWRSSEALR 290
Db 274 SSG-----SSRGTFRPR-----SLKRGSKPSASSASLEKRMKMWVSQIT 313
QY 291 QREYAEALLRGRKLARSALILSAPAIWAPYCLFTIVLSTYPTERTPRPKSVVYSIAFWLQW 350
Db 314 QR--FRLSRDKKVAKSLAIIIVIFGLCWAPYTLMIIRAACHGRCIP-DYWYETSFLLW 370
QY 351 FNSFVNPFLYPLCHRRFQKAFWKILCVTK 379
Db 371 ANSAVNPVLYPLCHYSFRFAFTKLLCPQK 399

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RESULT 13

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US-09-524-162-2
; Sequence 2, Application US/09524162
; Patent No. 6355452
; GENERAL INFORMATION:
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: HUMAN HISTAMINE H3 GENE VARIANT-2
; FILE REFERENCE: GP-70681
; CURRENT APPLICATION NUMBER: US/09/524,162
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-524-162-2

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Query Match 30.3%; Score 621.5; DB 3; Length 351;
Best Local Similarity 38.3%; Pred. No. 8.9e-44;
Matches 141; Conservative 44; Mismatches 110; Indels 73; Gaps 8;

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QY 18 LAPLSSAPALMGNVAVILAFVVDRLNRHSNYFFLNLAISDPLVGLIPIPLYPVL 77
Db 37 LAALMALIVATVGLNALVMAFAVDSSLRQNNFFLNLAISDPLVG----- 84
QY 78 FNNPFGSICMFWLITDYLLCTASVYNIIVLSYDRYQSVNVAQHTGIMKIVAOV 137
Db 85 -RWTFGRGLKLVVDVLLCTSSAFNIVLSYDRFLSVTRAVSRAQGGDTRAVRQML 143
QY 138 AVWILAFVNGPMLASDSWK-----NSTNTKCEPGFVTEWYILITIMLLEFLLPVISV 192
Db 144 LVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCVAEFFYNNYFLITASTLEFFTPFLSV 200
QY 193 AYFNVOIYWSLWKRRALSRCPSHAGFTSSASGHLHRAGVACRTSNPGLKESASRHS 252
Db 201 TFFNLSIYNIQRTRL-----RLDGAREAGPEPPPEAQPSP 239
QY 253 ESRRKSSILVSLRTHMNSSITAFKVGFWRSSEALRQREVAELL-RGRKLARSALIL 311
Db 240 PPP-----CCW-----GCWQKGHEAMPLHRKVAKSLAVIV 270
QY 312 SFAIWCAPYCLFTIVLSTYPTERTPRPKSVVYSIAFWLQWNSFVNPFLYPLCHRRFQKAF 371
Db 271 SIFGLCWAPYTLMIIRAACHGCV-P-DYWYETSFLLWANSVNPVLYPLCHHSFRFAF 329
QY 372 WKILCVTK 379
Db 330 TKLLCPQK 337

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RESULT 14

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US-08-985-090-5
; Sequence 5, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D. J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-090-5

```

Query Match 28.4%; Score 582.5; DB 2; Length 362;

Best Local Similarity 37.7%; Pred. No. 1.6e-40;

Matches 137; Conservative 45; Mismatches 118; Indels 63; Gaps 10;

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QY 65 GLISIPLYIPHLVLP-NNPNFGSICMFWLITDYLLCTASVYNIIVLSYDRYQSVNVAQV 123
Db 1 GAFCIPLYPVPLTGRWTFGRGLKLVVDVLLCASSVFNIVLSYDRFLSVTRAVSYR 60
QY 124 AQHTGIMKIVAOVAVILAFVNGPMLASDSWK-----NSTNTKCEPGFVTEWYILT 178
Db 61 AQGGDTRAVRQMLVAVLAFVLPAIL---SWEYLSGGSSIPEGHCYABEFFYNNYFLI 117
QY 179 ITMLLEFLLPVISVAYFNVOIYWSLWKRRAL-----SRCPSHAGFTTS 222
Db 118 SASTLEFFTPFLSVTFNLSIYNIQRTRLRDGREGAGPEPPDAQPSPPPPSCWG 177
QY 223 SSASGH-----LHRAGVACRTSNPGLK-----ESAASRHSERPR 256
Db 178 CWPKGHEAMPLHRYGVG--EAGPGVEAGEAALGGGGGGAAGPTSSSGSSSRGTFRPR 235
QY 257 RKSSILVSLRTHMNSSITAFKVGFWRSSEALRQREVAELLRGRKLARSALILSAPAI 316
Db 236 -----SLKRGSKPSASSASLEKRMKMWVSQITQR--FRLSRDKKVAKSLAIIIVIFGL 286
QY 317 CWAPYCLFTIVLSTYPTERTPRPKSVVYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKILC 376
Db 287 CWAPYTLMIIRAACHGRCIP-DYWYETSFLLWANSVNPVLYPLCHYSFRFAFTKLLC 345
QY 377 VTK 379
Db 346 PQK 348

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RESULT 15

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US-09-165-543-32
; Sequence 32, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D. J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39

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Result No.	Score	Query Match	Length	DB	ID	Description
1	1370.5	66.9	390	9	US-09-812-216-2	Sequence 2, Appli
2	1370.5	66.9	390	9	US-09-910-411-2	Sequence 2, Appli
3	1370.5	66.9	390	10	US-09-875-076-14	Sequence 14, Appli
4	1370.5	66.9	390	10	US-09-876-252-14	Sequence 14, Appli
5	1370.5	66.9	390	10	US-09-852-165-2	Sequence 2, Appli
6	1370.5	66.9	390	10	US-09-891-138A-6	Sequence 6, Appli
7	1370.5	66.9	390	13	US-10-052-193-2	Sequence 2, Appli
8	1370.5	66.9	390	14	US-10-325-567A-629	Sequence 629, Appli
9	1370.5	66.9	390	14	US-10-325-983-14	Sequence 14, Appli
10	1370.5	66.9	390	14	US-10-254-769-2	Sequence 2, Appli
11	1370.5	66.9	390	14	US-10-393-807-14	Sequence 14, Appli
12	1370.5	66.9	390	15	US-10-417-820A-14	Sequence 14, Appli
13	1370.5	66.9	390	15	US-10-349-253A-2	Sequence 2, Appli

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Db      61  DFFVGVISIPYIPIHTLFEWDFGKEICVFWLTTDYLLCTASVYNIIVLISYDRYLSVSNV 120
QY      121  SYRAQHTGINKIYVAVWVWILAFVNGPMILASDSKWSSTNTKDCPEPGVTWYILIT 180
Db      121  SYRTQHTGVLKIVTLVAVWVWILAFVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178
QY      - 181  MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPESHAGFSTTSSASGHLHRAGVACRTSN 240
Db      179  SFLEFVLPVLVAYFNNIYWSLWKRDHLSCQSHFGLTAVSSNICHSFRGLSRRSL 238
QY      241  PGLKESAASHRSRSPRRKSSILVSLRTHMNSSITAFKVGSMRSESAALRQREYAEELRG 300
Db      239  SASTEVPASPHSRQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVALLRA 298
QY      301  RKLARSAILLSAFACWAPYCLFTIVLSTYPTERPCKSVWYSIAFWLQWNSFVNPLY 360
Db      299  RRLAKSLAILLGVFAVCWAPYSFLTIVLSFYSSATGPKSVWYRIAFWLOQWNSFVNPLY 358
QY      361  PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391
Db      359  PLCHRRFQKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 2
US-09-910-411-2
; Sequence 2, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-910-411-2

Query Match      66.9%; Score 1370.5; DB 9; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.2e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY      1  MSESNSGILPPAAQVPLAFMSSPAFMVGNVAVLAFVVDNRHRSNYEFLNLAIS 60
Db      1  MPDNTNSTINLSLSTRTVTLFAFFMSLVAFALMGNALVILAFVVDNLRHRSYFFFLNLAIS 60
QY      61  DFLVGLGISIPYIPIHVLFWNNFGSGICMEFWLITDYLLCTASVYNIIVLISYDRYQSVSNV 120
Db      61  DFFVGVISIPYIPIHTLFEWDFGKEICVFWLTTDYLLCTASVYNIIVLISYDRYLSVSNV 120
QY      121  SYRAQHTGINKIYVAVWVWILAFVNGPMILASDSKWSSTNTKDCPEPGVTWYILIT 180
Db      121  SYRTQHTGVLKIVTLVAVWVWILAFVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178
QY      181  MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPESHAGFSTTSSASGHLHRAGVACRTSN 240
Db      179  SFLEFVLPVLVAYFNNIYWSLWKRDHLSCQSHFGLTAVSSNICHSFRGLSRRSL 238
QY      241  PGLKESAASHRSRSPRRKSSILVSLRTHMNSSITAFKVGSMRSESAALRQREYAEELRG 300

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Db      239  SASTEVPASPHSRQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVALLRA 298
QY      301  RKLARSAILLSAFACWAPYCLFTIVLSTYPTERPCKSVWYSIAFWLQWNSFVNPLY 360
Db      299  RRLAKSLAILLGVFAVCWAPYSFLTIVLSFYSSATGPKSVWYRIAFWLOQWNSFVNPLY 358
QY      361  PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391
Db      359  PLCHRRFQKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 3
US-09-875-076-14
; Sequence 14, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-076-14

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Query Match 66.9%; Score 1370.5; DB 10; Length 390;  
Best Local Similarity 68.1%; Pred. No. 1.2e-117;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGTLPPAAQVPLAFMSSFAFAIMVGNVILAFVVDNRNLRHRSNYFFFLNLALS 60  
DB 1 MPTDNTINLSLSTRVTLTAFFMSLVAFALMGNALVILAFVVDNRNLRHRSNYFFFLNLALS 60

QY 61 DFLVGLISIPLYIPHVLNFMNFGSGICMFWLITDYLCTASVYINVLISYDRYSQSVNAV 120  
DB 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDTLLCTASVYINVLISYDRYSQSVNAV 120

QY 121 SYRAQHTGIMKIVAOQVAVILAFVNGPMLASDSKNSNTKDCPFGFTWETWILIT 180  
DB 121 SYRTQHTGVLKIVLAVVAVVILAFVNGPMLTAVSVESKDEGS--ECEPGFFSEWILAIT 178

QY 181 MLEFLLPVISVAYFNQIYVSLWKRRALSRCPSHAGSTTSSASGHLHRAGVACRTSN 240  
DB 179 SFLEFVIPVILVAYFNMIYVSLWKRDHLSCQSHPLGTAVSSNICGHSFRGLSRSL 238

QY 241 PGLKESAAHRHSPRRKSSILVSLRTHMNSSITAFKVGSPWRSSAALRQREYAEELRG 300  
DB 239 SASTEVPAFSEHQRQRKSSLMPSRTKMSNTTASKMGSPSQSDSVLHQHVEHVELLA 298

QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPTPRTERPKSVWYISAFWLQWNSFVNPLY 360  
DB 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPLY 358

QY 361 PLCHRRFOKAFKILCVTKWPAISO-NQSVSS 391  
DB 359 PLCHRRFOKAFKILCVTKWPAISO-NQSVSS 390

RESULT 4  
US-09-876-252-14  
; Sequence 14, Application US/09876252  
; Publication No. US20030018182A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Lehmann-Bruinema, Karin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Receptor  
; FILE REFERENCE: AREN-0054  
; CURRENT APPLICATION NUMBER: US/09/876,252  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,951  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/152,524  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/151,114  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/108,029  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,127  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,131  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/141,448  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/156,555  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,634  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,653  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/157,280  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,294  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,281  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,282  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/156,633  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 146  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 14  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-876-252-14

Query Match 66.9%; Score 1370.5; DB 10; Length 390;  
Best Local Similarity 68.1%; Pred. No. 1.2e-117;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGTLPPAAQVPLAFMSSFAFAIMVGNVILAFVVDNRNLRHRSNYFFFLNLALS 60  
DB 1 MPTDNTINLSLSTRVTLTAFFMSLVAFALMGNALVILAFVVDNRNLRHRSNYFFFLNLALS 60

QY 61 DFLVGLISIPLYIPHVLNFMNFGSGICMFWLITDYLCTASVYINVLISYDRYSQSVNAV 120  
DB 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDTLLCTASVYINVLISYDRYSQSVNAV 120

QY 121 SYRAQHTGIMKIVAOQVAVILAFVNGPMLASDSKNSNTKDCPFGFTWETWILIT 180  
DB 121 SYRTQHTGVLKIVLAVVAVVILAFVNGPMLTAVSVESKDEGS--ECEPGFFSEWILAIT 178

QY 181 MLEFLLPVISVAYFNQIYVSLWKRRALSRCPSHAGSTTSSASGHLHRAGVACRTSN 240  
DB 179 SFLEFVIPVILVAYFNMIYVSLWKRDHLSCQSHPLGTAVSSNICGHSFRGLSRSL 238

QY 241 PGLKESAAHRHSPRRKSSILVSLRTHMNSSITAFKVGSPWRSSAALRQREYAEELRG 300  
DB 239 SASTEVPAFSEHQRQRKSSLMPSRTKMSNTTASKMGSPSQSDSVLHQHVEHVELLA 298

QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPTPRTERPKSVWYISAFWLQWNSFVNPLY 360  
DB 299 RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPLY 358



Db 1 MPDNTNSTINLSUSTRVTTLTAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSYFFFLNLAIS 60  
Qy 61 DFLVGLISIPYIPHLVFNWNGSGICMFWLITDYLCTASVYVNIIVLISYDRYQSVSNV 120  
Db 61 DFFVGVISIPYIPHLTPEWDFGKEICVFWLITDYLCTASVYVNIIVLISYDRYLSVSNV 120  
Qy 121 SYRAQHTGIMKIQAQVAVWILAFVNGPMLASDWSKNSTNTKDCBPGFVTEWYILIT 180  
Db 121 SYRTQHTGVLKIVLMAVWVLAFLVNGPMLVSVESWDEGS--ECPGPFSEWYILAIT 178  
Qy 181 MLEFLLPVIISVAVFNVOIYNSLWKRRLSRCPHAGFSTTSSASGHLHRAGVACRTSN 240  
Db 179 SFLEFVPIVILVAVFNMMIYNSLWKRDLHLSRCQSHPLGTAVSSNICHSGFRGLSSRSL 238  
Qy 241 PGLKESAAARHSESPRRKSSILVLRTHMNSITAFKVGSPWRSSESAALRQREYAEELRG 300  
Db 239 SASTEVPAFHSERQRKSSLMFSSRTTQNSNTIASKGFSQSDVALHQREHVELLRA 298  
Qy 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYISIAFWLQWFNFSFVNPLY 360  
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLMQWFNFSFVNPLY 358  
Qy 361 PLCHRRFOKAFWKILCVTKWPALSO-NQSVSS 391  
Db 359 PLCHKRFOKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 8  
US-10-225-567A-629  
; Sequence 629, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.  
; FILE REFERENCE: 1920-4-4  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 629  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-629

Query Match 66.9%; Score 1370.5; DB 14; Length 390;  
Best Local Similarity 68.1%; Pred. No. 1.2e-117;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
Qy 1 MSENSTGILPPAAQVPLAFMSSPAFAIMVGNVAVILAFVVDKNLRHRSYFFFLNLAIS 60  
Db 1 MPDNTNSTINLSUSTRVTTLTAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSYFFFLNLAIS 60  
Qy 61 DFLVGLISIPYIPHLVFNWNGSGICMFWLITDYLCTASVYVNIIVLISYDRYQSVSNV 120  
Db 61 DFFVGVISIPYIPHLTPEWDFGKEICVFWLITDYLCTASVYVNIIVLISYDRYLSVSNV 120  
Qy 121 SYRAQHTGIMKIQAQVAVWILAFVNGPMLASDWSKNSTNTKDCBPGFVTEWYILIT 180  
Db 121 SYRTQHTGVLKIVLMAVWVLAFLVNGPMLVSVESWDEGS--ECPGPFSEWYILAIT 178  
Qy 181 MLEFLLPVIISVAVFNVOIYNSLWKRRLSRCPHAGFSTTSSASGHLHRAGVACRTSN 240  
Db 179 SFLEFVPIVILVAVFNMMIYNSLWKRDLHLSRCQSHPLGTAVSSNICHSGFRGLSSRSL 238  
Qy 241 PGLKESAAARHSESPRRKSSILVLRTHMNSITAFKVGSPWRSSESAALRQREYAEELRG 300

Db 239 SASTEVPAFHSERQRKSSLMFSSRTTQNSNTIASKGFSQSDVALHQREHVELLRA 298  
Qy 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYISIAFWLQWFNFSFVNPLY 360  
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLMQWFNFSFVNPLY 358  
Qy 361 PLCHRRFOKAFWKILCVTKWPALSO-NQSVSS 391  
Db 359 PLCHKRFOKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 9  
US-10-272-983-14  
; Sequence 14, Application US/10272983  
; Publication No. US20030148450A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/272,983  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: US/09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-272-983-14

Query Match 66.9%; Score 1370.5; DB 14; Length 390;  
Best Local Similarity 68.1%; Pred. No. 1.2e-117;  
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;  
Qy 1 MSENSTGILPPAAQVPLAFMSSPAFAIMVGNVAVILAFVVDKNLRHRSYFFFLNLAIS 60  
Db 1 MPDNTNSTINLSUSTRVTTLTAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSYFFFLNLAIS 60  
Qy 61 DFLVGLISIPYIPHLVFNWNGSGICMFWLITDYLCTASVYVNIIVLISYDRYQSVSNV 120  
Db 61 DFFVGVISIPYIPHLTPEWDFGKEICVFWLITDYLCTASVYVNIIVLISYDRYLSVSNV 120  
Qy 121 SYRAQHTGIMKIQAQVAVWILAFVNGPMLASDWSKNSTNTKDCBPGFVTEWYILIT 180  
Db 121 SYRTQHTGVLKIVLMAVWVLAFLVNGPMLVSVESWDEGS--ECPGPFSEWYILAIT 178  
Qy 181 MLEFLLPVIISVAVFNVOIYNSLWKRRLSRCPHAGFSTTSSASGHLHRAGVACRTSN 240  
Db 179 SFLEFVPIVILVAVFNMMIYNSLWKRDLHLSRCQSHPLGTAVSSNICHSGFRGLSSRSL 238

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QY 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGSWRSESAALRQREYAEALLRG 300
Db 239 SASTEPASPHSRQRKSKSLMFSSRTKNSNTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391
Db 359 PLCHKRFQKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 10
US-10-354-769-2
; Sequence 2, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-769-2

Query Match 66.9%; Score 1370.5; DB 14; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.2e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMLSSFAIMVGNVILAFVVDVDRNLHRHSNTFFFLNLALS 60
Db 1 MPDTNSTINLSLSTRVTLAFPMLSLVAFAIMLGNALVILAFVVDKRLHRSSYFFFLNLALS 60
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVSNV 120
Db 61 DFFVGVISIPLYIPHLTFEWDGKEICVFPLTDDYLLCTASVYNIIVLISYDRYLSVSNV 120
QY 121 SYRAOHTGIMKIVAOVAVMILAFVNGPMILASDKNSNTKCEPGFVTEWYILTIT 180
Db 121 SYRTQHTGVLKIVLMVAVVILAFVNGPMILVSSWKDEGS--ECEPGFFSEWYILAIT 178
QY 181 MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPESHAGFTTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVIPVLVAYFNMNIYWSLWKRDHLSCQSHPLGTAVSSNICGHSFRGLSSRRSL 238
QY 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGSWRSESAALRQREYAEALLRG 300
Db 239 SASTEPASPHSRQRKSKSLMFSSRTKNSNTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391
Db 359 PLCHKRFQKAFKIFCIKQPLPSQHSRSVSS 390
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RESULT 11
US-10-393-807-14
; Sequence 14, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-807-14

Query Match 66.9%; Score 1370.5; DB 14; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.2e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMLSSFAIMVGNVILAFVVDVDRNLHRHSNTFFFLNLALS 60
Db 1 MPDTNSTINLSLSTRVTLAFPMLSLVAFAIMLGNALVILAFVVDKRLHRSSYFFFLNLALS 60
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVSNV 120
Db 61 DFFVGVISIPLYIPHLTFEWDGKEICVFPLTDDYLLCTASVYNIIVLISYDRYLSVSNV 120
QY 121 SYRAOHTGIMKIVAOVAVMILAFVNGPMILASDKNSNTKCEPGFVTEWYILTIT 180
Db 121 SYRTQHTGVLKIVLMVAVVILAFVNGPMILVSSWKDEGS--ECEPGFFSEWYILAIT 178
QY 181 MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPESHAGFTTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVIPVLVAYFNMNIYWSLWKRDHLSCQSHPLGTAVSSNICGHSFRGLSSRRSL 238
QY 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSSITAFKVGSWRSESAALRQREYAEALLRG 300
Db 239 SASTEPASPHSRQRKSKSLMFSSRTKNSNTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPYCLFTTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFY 358
QY 361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391
Db 359 PLCHKRFQKAFKIFCIKQPLPSQHSRSVSS 390
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Db      359  RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358
Qy      361  PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 391
Db      359  PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 390

RESULT 13
US-10-417-820A-14
; Sequence 14, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-820A-14

Query Match      66.9%; Score 1370.5; DB 15; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.2e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy      1  MSENSTGILPPAAQVPLAFMSSPAPAIMVGNVAVILAFVVDNRNLRHRSYFFLNLAIS 60
Db      1  MPDNTNINLSLSTRVTLAFPMSLVAFALMGNALVILAFVVDNRNLRHRSYFFLNLAIS 60
Qy      61  DFLVGLISIPLYIPHLVFNMFNGSGICMFWLITDYLCTASVYVNIIVLSYDRYOSVSNV 120
Db      61  DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDTYLLCTASVYVNIIVLSYDRYOSVSNV 120
Qy      121 SYRAQHTGIMKIQAQVAVILAFVNGPMLASDSWKNSTNTKDCBPGFTWYILIT 180
Db      121 SYRTQHTGVILKIVTLMAVAVVLAFLVNGPMLVSESWKDEGS--ECPGFFSEWYILAIT 178
Qy      181 MLLEFLPLVIVSVYFVNOIYWSLWKRRLSCPSPHAGFTSTSSASGHLHRAGVACRTSN 240
Db      179 SFLEFVPIVLVAFVNMNIYWSLWKRDLHRCQHPGLTAVSSNICHSFGRISRRSL 238
Qy      241 PGLKESAAHRHSESPRRKSSILVLRTHMNSSITAFKVGSPFRSSEALRQREYAEILRG 300
Db      239 SASTVEVPASFSERQRKSSLMFSSRTKMSNTTASKMGSPSQSDSVLHQHREVELLRA 298
Qy      301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYRIAFWLQWNSFVNPLY 360
Db      299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358
Qy      361  PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 391
Db      359  PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 390

US-10-349-253A-2
; Sequence 2, Application US/10349253A
; Publication No. US20040043393A1
; GENERAL INFORMATION:
; APPLICANT: Aubart, Kelly
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Graybill, Todd
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Morrow, Dwight
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C2
; CURRENT APPLICATION NUMBER: US/10/349,253A
; CURRENT FILING DATE: 2003-01-21
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-349-253A-2

Query Match      66.9%; Score 1370.5; DB 15; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.2e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy      1  MSENSTGILPPAAQVPLAFMSSPAPAIMVGNVAVILAFVVDNRNLRHRSYFFLNLAIS 60
Db      1  MPDNTNINLSLSTRVTLAFPMSLVAFALMGNALVILAFVVDNRNLRHRSYFFLNLAIS 60
Qy      61  DFLVGLISIPLYIPHLVFNMFNGSGICMFWLITDYLCTASVYVNIIVLSYDRYOSVSNV 120
Db      61  DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDTYLLCTASVYVNIIVLSYDRYOSVSNV 120
Qy      121 SYRAQHTGIMKIQAQVAVILAFVNGPMLASDSWKNSTNTKDCBPGFTWYILIT 180
Db      121 SYRTQHTGVILKIVTLMAVAVVLAFLVNGPMLVSESWKDEGS--ECPGFFSEWYILAIT 178
Qy      181 MLLEFLPLVIVSVYFVNOIYWSLWKRRLSCPSPHAGFTSTSSASGHLHRAGVACRTSN 240
Db      179 SFLEFVPIVLVAFVNMNIYWSLWKRDLHRCQHPGLTAVSSNICHSFGRISRRSL 238
Qy      241 PGLKESAAHRHSESPRRKSSILVLRTHMNSSITAFKVGSPFRSSEALRQREYAEILRG 300
Db      239 SASTVEVPASFSERQRKSSLMFSSRTKMSNTTASKMGSPSQSDSVLHQHREVELLRA 298
Qy      301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYRIAFWLQWNSFVNPLY 360
Db      299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLY 358
Qy      361  PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 391
Db      359  PLCHRRFQKAFWKILCVTKWPALSO-NOSVSS 390

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RESULT 14
US-10-696-673-2
; Sequence 2, Application US/10696673
; Publication No. US20040105846A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsen
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wood, Linda S
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: PHR0025-101/00231REGUS.1 DV1
; CURRENT APPLICATION NUMBER: US/10/696,673
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 60/203,108
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: US 09/852,165
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-696-673-2

Query Match      66.9%; Score 1370.5; DB 16; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.2e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDNRNLRHSNYFFFLNLAIS 60
DB 1 MPDNTNINLSLSTRVTLAFVMSLVAFAIMLGNALVILAFVVDKLRHSRFFFLNLAIS 60

QY 61 DFLVGLISIPLYPHLVFNMFSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVNAV 120
DB 61 DPFVGVISIPLYPHLVFNMFSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVNAV 120

QY 121 SYRAQHTGIMKIQAQVAVWILAFVNGPMLASDWSKNTWKDCPEGFVTEWYILTT 180
DB 121 SYRTQHTGVLKIVTLWAVVWILAFVNGPMLVSESWKDEGS--ECEPGFFSEWYILAIT 178

QY 181 MLLEFLLPVISVAYFNVOIYWSLWKRRALSRCPHAGFTTSSASGHLHRAGVACRTSN 240
DB 179 SPLEFVIPVILVAYFNWNIYWSLWKRDHLSCQSHPLGLTAVSSNICHSFRGLSSRRSL 238

QY 241 PGLKESAAHRHSESPRRKSSILVSLRTHMNSSITAFKVGSPWRSESAALRQREYAE LLRG 300
DB 239 SASTEVPAFSHBRQRKSSLMPSRTKWNNTIASKMGFSQSDSVALHQREHVELLRA 298

QY 301 RKLARSAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLLY 360
DB 299 RRLAKSLAILLGFAVCAWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLOWFNSFVNPFLLY 358

QY 361 PLCHRRFQKAFWKILCVTKWPALSO--NOSVSS 391
DB 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 15
US-10-723-955-14
; Sequence 14, Application US/10723955
; Publication No. US20040110238A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lin, I-Lin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lehman-Bruinsma, Karin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Gore, Martin

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; APPLICANT: White, Carol
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; FILE REFERENCE: 7.US29.CON
; CURRENT APPLICATION NUMBER: US/10/723,955
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 10/417,820
; PRIOR FILING DATE: 2003-4-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-955-14

Query Match      66.9%; Score 1370.5; DB 16; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.2e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDNRNLRHSNYFFFLNLAIS 60
DB 1 MPDNTNINLSLSTRVTLAFVMSLVAFAIMLGNALVILAFVVDKLRHSRFFFLNLAIS 60

QY 61 DFLVGLISIPLYPHLVFNMFSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVNAV 120
DB 61 DPFVGVISIPLYPHLVFNMFSGICMFWLITDYLLCTASVYNIIVLISYDRYQSVNAV 120

QY 121 SYRAQHTGIMKIQAQVAVWILAFVNGPMLASDWSKNTWKDCPEGFVTEWYILTT 180
DB 121 SYRTQHTGVLKIVTLWAVVWILAFVNGPMLVSESWKDEGS--ECEPGFFSEWYILAIT 178

QY 181 MLLEFLLPVISVAYFNVOIYWSLWKRRALSRCPHAGFTTSSASGHLHRAGVACRTSN 240
DB 179 SPLEFVIPVILVAYFNWNIYWSLWKRDHLSCQSHPLGLTAVSSNICHSFRGLSSRRSL 238

QY 241 PGLKESAAHRHSESPRRKSSILVSLRTHMNSSITAFKVGSPWRSESAALRQREYAE LLRG 300
DB 239 SASTEVPAFSHBRQRKSSLMPSRTKWNNTIASKMGFSQSDSVALHQREHVELLRA 298

QY 301 RKLARSAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLLY 360
DB 299 RRLAKSLAILLGFAVCAWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLOWFNSFVNPFLLY 358

QY 361 PLCHRRFQKAFWKILCVTKWPALSO--NOSVSS 391
DB 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRSVSS 390

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Search completed: April 6, 2005, 19:35:28  
Job time : 79 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 19:04:58 ; Search time 26 Seconds  
(without alignments)  
1446.952 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSESNTGILPPAAQVPLAF.....KKILCVTKMPALSNQSVSS 391

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1370.5	66.9	390	2 UC7566	histamine H4 recep
2	413	20.2	460	2 S09508	muscarinic acetyl
3	413	20.2	460	2 A24325	muscarinic acetyl
4	410.5	20.0	531	2 J70531	muscarinic acetyl
5	410.5	20.0	590	2 S01114	muscarinic acetyl
6	410	20.0	460	2 I51837	muscarinic recepto
7	410	20.0	460	2 A23514	muscarinic acetyl
8	409.5	20.0	590	2 S47572	muscarinic acetyl
9	403	19.7	589	2 A29476	muscarinic acetyl
10	402.5	19.7	590	2 S10128	muscarinic acetyl
11	402	19.6	589	2 B29514	muscarinic acetyl
12	401	19.5	639	2 A55019	muscarinic acetyl
13	400	19.5	460	2 A31897	muscarinic acetyl
14	399.5	19.5	532	2 J70530	muscarinic acetyl
15	392.5	19.2	477	2 S71323	alpha-1A adrenerg
16	392	19.1	490	2 A35546	muscarinic acetyl
17	390.5	19.1	400	2 G00013	D3 dopamine recep
18	390.5	19.1	501	2 JH0447	alpha-1A-adrenerg
19	389.5	19.0	400	2 G01977	D3 dopamine recep
20	389.5	19.0	515	2 A40491	alpha-1-adrenerg
21	388.5	19.0	491	2 A41632	histamine H1 recep
22	388.5	19.0	572	2 J13969	alpha-1A-adrenerg
23	386.5	18.9	487	2 J24295	histamine H1 recep
24	385.5	18.8	488	2 I56507	histamine H1 recep
25	384.5	18.8	517	2 A45121	alpha-1B adrenerg
26	382.5	18.7	560	2 A38731	muscarinic acetyl
27	382	18.6	466	2 S10127	muscarinic acetyl
28	380.5	18.6	466	2 S10126	muscarinic acetyl
29	380.5	18.6	501	2 T18863	hypothetical prote

30	380	18.6	432	2 I50829	alpha-2-adrenocept
31	380	18.6	466	2 A40972	muscarinic acetyl
32	379.5	18.5	466	2 JH0197	muscarinic acetyl
33	379.5	18.5	466	2 S10856	muscarinic acetyl
34	379.5	18.5	515	2 J21525	alpha-1B-adrenerg
35	379	18.5	486	2 J21415	histamine H1 recep
36	377.5	18.4	379	2 J21415	serotonin receptor
37	376	18.4	478	2 C29514	muscarinic acetyl
38	374.5	18.3	479	2 S33786	muscarinic acetyl
39	369.5	18.0	466	2 A23386	muscarinic acetyl
40	367.5	17.9	366	2 A47321	serotonin receptor
41	367	17.9	484	2 S48657	muscarinic acetyl
42	366.5	17.9	484	2 S58868	G protein-coupled
43	366	17.9	466	2 A35375	alpha-1-adrenerg
44	364.5	17.8	366	2 A47385	serotonin receptor
45	360.5	17.6	366	2 S26048	serotonin receptor

## ALIGNMENTS

### RESULT 1

UC7566 histamine H4 receptor, HH4R - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-2001 #sequence\_revision 30--Jun-2001 #text\_change 09-Jul-2004  
C:Accession: UC7566  
R:Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.  
Biochem. Biophys. Res. Commun. 279, 615-620, 2000  
A>Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.  
A:Reference number: UC7566; MUID: 20568725; PMID:11118334  
A:Contents: Leukocyte  
A:Accession: UC7566  
A:Molecule type: mRNA  
A:Residues: 1-390 <NA>  
A:Cross-references: UNIPROT:Q9H3N8; DDBJ:AB045370  
C:Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled  
C:Genetics:  
A:Gene: HH4R  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	Score	Length
Best Local Similarity	66.9%	390;
Matches	267; Conservative	40; Mismatches 82; Indels 3; Gaps 2;
QY	1	MSESNTGILPPAAQVPLAFMSFPAIWNAGNAVILAFVDRNLRRHSNYFLNLAI
DB	1	MPDNTSTNLSTRTVTLAFMSLVAFAIMGNALVILAFVDDKVLRRSSYFLNLAI
QY	61	DFVLGLISPIYIYHVLFNMPGSGICMPULITDYLLCTASAVNIVLISYRQSVSNV
DB	61	DFPVGIVISPIYIYHVLFNMPGSGICMPULITDYLLCTASAVNIVLISYRQSVSNV
QY	121	SYRQHTGIMKIVQMVAVIILAFVNGPMLIASDSWKNSTNTDCDEGPTWYLLIT
DB	121	SYRQHTGIVLIVLMAVAVIILAFVNGPMLIASDSWKNSTNTDCDEGPTWYLLIT
QY	181	MLLEFLLEPVISAVYFNVOIYSLMKRRALSRCPHAGFSTTSSASGHLRAGVACRTSN
DB	179	SFLFELVIVLIVAFVFNMIYSLMKRDLRSQSHPGTLAVSSNIGHSFGRILSRSL
QY	241	PGLESASARSESPRRSSILVSLRTMNSITAFKVGSRWRESALRREYELLRG
DB	239	SASTEVPAFSESRORRSSLFSSRTKMSNTLASIKGSQSDSVALLHREHLLRA
QY	301	RKLARSIAIILSAPAIICWAPCLFTIYVSTPRTERPSSVWYSAIFMOWFNSFVNPFLY
DB	299	RRLKSLAIILGVAVACAPYSLFTIYVSTPRTERPSSVWYSAIFMOWFNSFVNPFLY
QY	361	PLCHRRFOKAFWKILCVTKMPALSQ-NQSVSS 391
DB	359	PLCHRRFOKAFWKILCVTKMPALSQ-NQSVSS 390

## RESULT 2

muscarinic acetylcholine receptor M1 - human  
S09508  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C/Accession: S09508; S06327; S04326  
R/Chapman, C.G.; Browne, M.J.  
Nucleic Acids Res. 18, 2191, 1990  
A/Title: Isolation of the human m1 (hml) muscarinic acetylcholine receptor gene by PCR  
A/Reference number: S09508; MUID:50245684; PMID:2336407  
A/Accession: S09508  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Accession: S09508  
A/Molecule type: DNA  
A/Residues: 1-460 <CNA>  
A/Cross-references: UNIPROT:P11229; EMBL:X52068; NID:334450; PIDN:CAA36291.1; PID:G34451  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990  
R/Allard, W.J.; Sigal, I.S.; Dixon, R.A.F.  
Nucleic Acids Res. 15, 10604, 1987  
A/Title: Sequence of the gene encoding the human M1 muscarinic acetylcholine receptor.  
A/Reference number: S06327; MUID:88096607; PMID:3697105  
A/Accession: S06327  
A/Molecule type: DNA  
A/Residues: 1-460 <ALL>  
A/Cross-references: GB:X00508; GB:M35128; NID:9297405; PIDN:CAA68560.1; PID:9297406  
R/Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.  
EMBO J. 6, 3923-3929, 1987  
A/Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of three human muscarinic acetylcholine receptor subtypes.  
A/Reference number: S04326; MUID:88166632; PMID:3443095  
A/Accession: S04326  
A/Molecule type: DNA  
A/Residues: 1-172, 'M', 174-460 <PER>  
A/Cross-references: EMBL:X15263; NID:G32317; PIDN:CAA3334.1; PID:G32318  
A/Suprafamily: vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
F/25-50/Domain: transmembrane #status predicted <TM1>  
F/62-93/Domain: transmembrane #status predicted <TM2>  
F/100-121/Domain: transmembrane #status predicted <TM3>  
F/142-168/Domain: transmembrane #status predicted <TM4>  
F/187-209/Domain: transmembrane #status predicted <TM5>  
F/367-387/Domain: transmembrane #status predicted <TM6>  
F/402-420/Domain: transmembrane #status predicted <TM7>  
F/2,12/Binding site: carbonyl (Asn) (covalent) #status predicted

Query Match 20.2%; Score 413; DB 2; Length 460;

Best Local Similarity 27.4%; Pred. No. 9.7e-28; Mismatches 150; Indels 90; Gaps 19;

Matches 122; Conservative 84; Mismatches 150; Indels 90; Gaps 19;

QY 5 NSTGILPPAAQVPLAFL--MSSFAFAIVGNVAVIAPVVDRLRHRSNYFFLNLAI5D 61  
DB 12 NITVLAPEGKQPMQVAVIGITGGLSLATVGNLVLISFVNTLKTNNYFLLSLACAD 71  
QY 62 FLVGLISIPLYIPHYLF-NMNFSGGICMFLITDYLLCTASVYNYIVLISYDRQSSNAV 120  
DB 72 LIIGTFSMNLTYTYLLMGHVALGTLACDMLADYVSNASVNNLLISFDRFYSYTRPL 131  
QY 121 SYRAOHTGIMKIYAQVAV--MILAFVNGPMILASDSWKNSNTWK-----DCEPGVTW 174  
DB 132 SYRAKKT--PRRALMIGLMLVSEFVLMAPAIL--FWQYLVGERIVLAGQCTIQLISQP 186  
QY 175 YILITMLLEFLLPVISAIVFVNOIYWSLWK-----RAL-----SRCPHAGFSTTSS 224  
DB 187 IIFPGTAMAFYLPVTVMC--TLVWRIYRETNRAELALQGSSTPKGGSSSSSE 242  
QY 225 AS-----GHLHRAVACRT-----SNGLKESASRSSESPRRK 258  
DB 243 RSQPGAEGSPETPRGRCR--CCRAPRLLOAVSWKEEEDSGMSLTSSEGEPP--G 297  
QY 259 SSILVSL-----RTHMNSITAFKVSFMSSESA-----ALRQREY 294  
DB 298 SEVVIKMPVDPDAQAPKOPRPSSPYTKRPKRKREARAGKQKRGKEQLAKRTK 354  
QY 295 AELLGRKLARSALILSAFAICWAPYCLFTIVLSTYPRTERPKSVVYSIAFWLQWNSF 354

## RESULT 3

muscarinic acetylcholine receptor - pig  
A24325  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 09-Jul-2004  
C/Accession: A24325  
R/Kubo, T.; Fukuda, K.; Mikami, A.; Maeda, A.; Takahashi, H.; Mishina, M.; Haga, T.; Haga, T.  
Nature 323, 411-416, 1986  
A/Title: Cloning, sequencing and expression of complementary DNA encoding the muscarinic  
A/Reference number: A24325; MUID:87014801; PMID:3762692  
A/Accession: A24325  
A/Molecule type: mRNA  
A/Residues: 1-460 <KUB>  
A/Cross-references: UNIPROT:P04761; GB:X04413; NID:G1863; PIDN:CAA28003.1; PID:G1866  
C/Suprafamily: vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
F/25-50/Domain: transmembrane #status predicted <TM1>  
F/62-93/Domain: transmembrane #status predicted <TM2>  
F/100-121/Domain: transmembrane #status predicted <TM3>  
F/142-168/Domain: transmembrane #status predicted <TM4>  
F/187-209/Domain: transmembrane #status predicted <TM5>  
F/367-387/Domain: transmembrane #status predicted <TM6>  
F/402-420/Domain: transmembrane #status predicted <TM7>

Query Match 20.2%; Score 413; DB 2; Length 460;

Best Local Similarity 27.5%; Pred. No. 9.7e-28; Mismatches 154; Indels 84; Gaps 18;

Matches 122; Conservative 83; Mismatches 154; Indels 84; Gaps 18;

QY 5 NSTGILPPAAQVPLAFL--MSSFAFAIVGNVAVIAPVVDRLRHRSNYFFLNLAI5D 61  
DB 12 NITVLAPEGKQPMQVAVIGITGGLSLATVGNLVLISFVNTLKTNNYFLLSLACAD 71  
QY 62 FLVGLISIPLYIPHYLF-NMNFSGGICMFLITDYLLCTASVYNYIVLISYDRQSSNAV 120  
DB 72 LIIGTFSMNLTYTYLLMGHVALGTLACDMLADYVSNASVNNLLISFDRFYSYTRPL 131  
QY 121 SYRAOHTGIMKIYAQVAV--MILAFVNGPMILASDSWKNSNTWK-----DCEPGVTW 174  
DB 132 SYRAKKT--PRRALMIGLMLVSEFVLMAPAIL--FWQYLVGERIVLAGQCTIQLISQP 186  
QY 175 YILITMLLEFLLPVISAIVFVNOIYWSLWK-----RAL-----SRCPHAGFSTTSS 224  
DB 187 IIFPGTAMAFYLPVTVMC--TLVWRIYRETNRAELALQGSSTPKGGSSSSSE 242  
QY 225 AS-----GHLHRAVACRT-----SNGLKESASRSSESPRRK 258  
DB 243 RSQPGAEGSPETPRGRCR--CCRAPRLLOAVSWKEEEDSGMSLTSSEGEPP--G 297  
QY 259 SSILVSL-----RTHMNSITAFKVSFMSSESA-----LRQREY 297  
DB 298 SEVVIKMPVDPDAQAPKOPRPSSPYTKRPKRKREARAGKQKRGKEQLAKRTK 357  
QY 298 LRGKRLARSALILSAFAICWAPYCLFTIVLSTYPRTERPKSVVYSIAFWLQWNSFVN 357  
DB 358 VKEKKAFTLSAILLAFIYTWTFYNNMVLV--STFCDCDQVETLM--ELGWVLCVNSTIND 415  
QY 358 FLVPLCHRRPQKAFMKILCVTKW 380  
DB 416 MCYALCNKAFRDTF--RLILLCRW 437

## RESULT 4

muscarinic acetylcholine receptor M5 - rat  
J10531  
C/Species: Rattus norvegicus (Norway rat)

C>Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text\_change 09-Jul-2004  
C/Accession: J0531; A33354; C37121  
R/Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.  
Neuron 1, 403-410, 1988  
A>Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor  
A/Reference number: J0530; MUID:9016521; PMID:3272174  
A/Accession: J0531  
A/Molecule type: DNA  
A/Residues: 1-531 <BON>  
A/Cross-references: UNIPROT:P08911  
R/Lliso, C.F.; Thiemann, A.P.N.; Joho, R.; Barberis, C.; Birnbaumer, M.; Birnbaumer, L.  
J. Biol. Chem. 264, 7328-7337, 1989  
A>Title: Molecular cloning and expression of a fifth muscarinic acetylcholine receptor.  
A/Reference number: A33354; MUID:89214170; PMID:2540186  
A/Accession: A33354  
A/Molecule type: DNA  
A/Residues: 1-531 <LIA>  
A/Cross-references: GB:M2925; NID:9205311; PIDN:AAA1572.1; PID:9205312; GB:J04706  
A/Note: the nucleotide sequence for residues 101-120 and the translation 121-140 are not  
A/Note: the authors translated the codon CAG for residue 19 as Glu, AAC for residue 65 as  
R.Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Altken, A.; Harris, A.C.M.; Hulme, E.C.  
J. Biol. Chem. 265, 13702-13708, 1990  
A>Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues inv  
A/Reference number: A37121; MUID:90337982; PMID:2380182  
A/Accession: C37121  
A/Molecule type: preliminary  
A/Status: preliminary  
A/Residues: 66-128 <KOR>  
C/Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neurotr  
C/Suprafamily: vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
F:29-52/Domain: transmembrane #status predicted <TM1>  
F:66-86/Domain: transmembrane #status predicted <TM2>  
F:104-125/Domain: transmembrane #status predicted <TM3>  
F:146-168/Domain: transmembrane #status predicted <TM4>  
F:191-213/Domain: transmembrane #status predicted <TM5>  
F:443-463/Domain: transmembrane #status predicted <TM6>  
F:478-496/Domain: transmembrane #status predicted <TM7>  
F:7,12/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 20.0%; Score 410.5; DB 2; Length 531;  
Best Local Similarity 24.6%; Pred. No. 1.9e-27;  
Matches 122; Conservative 92; Mismatches 140; Indels 141; Gaps 15;

Qy 16 VPLALMSFAFAMGNVAVLAVVDRLNHRNYPFLNALISDFVLGLISILYIPH 75  
Db 30 ITIAVTVAVSLMTIVGNVLWISFKVNSQLTKVNNYLLSLACADLLIGFNMVLYTY 89  
Qy 76 VLF-NMNGSGICMFMLITDYLLCTASVYNIIVISYDRQSVSNVSYRAOHT---GIM 130  
Db 90 ILMGRWVLSGLACDLMLADLVASVSNVNLVVISFDRFSTIRPLTYRAKTPPRAGIM 149  
Qy 131 KIVAQVAVVILAFVNGPMILASDSW---KNSNTKDCPGEVTEVYILITMLLEF 185  
Db 150 IGLA-----WLVSFILMAPILC---MQLVGRKRVTPPEQIOQLSEPTITFGTAIAAF 201  
Qy 186 LLPVTSVAVFNVQIYWSLMKR-----RALSRCP----- 213  
Db 202 YIPVSVMTILYCRITRETERKTKDLADLQSDSVAAKKRBPORLLRSFSPSCPSIA 261  
Qy 214 ---SHAGFSTT---SSASGHLHRA-----GVACRTSNGLKESA----- 247  
Db 262 QREKQASWSSRRRTSTTGKTTQATDLSADMEKAEVOTTCSSYSSSEDEAKPTTDPVQ 321  
Qy 248 ---ASRHSESPARKSSILVSLTHNNSI---TAFVGSFWRSESAALR----- 290  
Db 322 MYVSEAKESPKESNTQETKETVNTRENSDYOTPKYFLSPAAAHLLKSKQCVAYKFR 381  
Qy 291 -----OREYAEILGRKRLAR 305  
Db 382 LVVKADQTOETNNGCRKVKIMECPSPVSKDPSTKGPDPNLSHOMTKRKRMVLYVKERKAAQ 441  
Qy 306 SLAILLSAFALCMAPYCLFTIYLVSTYPRTERPKSVWYSIAFWLQMFNSFVNPFLVPLGR 365

Db 442 TLSALLAFITITWTPYINMVLV-STFCOKCVPTLMH-LGYVLGVNSTRINPICALGNR 499  
Qy 366 RFQKAFPMKILCVTKW 380  
Db 500 TFRKTF-XLLLLCRW 513

RESULT 5  
S01114  
muscarinic acetylcholine receptor M2, glandular - pig  
N/Alternate names: muscarinic acetylcholine receptor III  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004  
C/Accession: S01114  
R/Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.  
FEBS Lett. 235, 257-261, 1988  
A>Title: Primary structure of porcine muscarinic acetylcholine receptor III and antago  
A/Reference number: S01114; MUID:88296835; PMID:3402600  
A/Accession: S01114  
A/Molecule type: DNA  
A/Residues: 1-590 <AKI>  
A/Cross-references: UNIPROT:P1483; EMBL:X12712; NID:91861; PIDN:CAA1215.1; PID:91862  
C/Suprafamily: vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme  
F:68-91/Domain: transmembrane #status predicted <TM1>  
F:105-125/Domain: transmembrane #status predicted <TM2>  
F:143-164/Domain: transmembrane #status predicted <TM3>  
F:185-207/Domain: transmembrane #status predicted <TM4>  
F:231-252/Domain: transmembrane #status predicted <TM5>  
F:493-513/Domain: transmembrane #status predicted <TM6>  
F:528-546/Domain: transmembrane #status predicted <TM7>

Query Match 20.0%; Score 410.5; DB 2; Length 590;  
Best Local Similarity 24.8%; Pred. No. 2.1e-27;  
Matches 125; Conservative 82; Mismatches 136; Indels 161; Gaps 16;

Qy 18 LAFILMSFAFAMGNVAVLAVVDRLNHRNYPFLNALISDFVLGLISILYIPH 77  
Db 71 IAFILGIALVITIGNIIIVAFVKNQKLVNNYFLSLACADLLIGVISNMVLYTY 130  
Qy 78 FN-NMNGSGICMFMLITDYLLCTASVYNIIVISYDRQSVSNVSYRAOHT---GIMKI 132  
Db 131 MRRALGSLACDLMLSDIVASVSNVNLVVISFDRFSTIRPLTYRAKTPPRAGIM 190  
Qy 133 VAQVAVVILAFVNGPMILASDSWKNSTNTKDCPGEVTEVYILITMLLEF 187  
Db 191 LA-----WVISFILMAPILC---FMQYVGRKRVTPPEQIOQLSEPTITFGTAIAAF 242  
Qy 188 PVISAVYNNVQIYWSLMGRRLSRCPSHAGF---STSSASGHLHRAVACRTSPGLKE 245  
Db 243 PVITMTI---LYRIYKETE-KRTKELAGLQASGTEAEAFVPTGSSSSCSYELQO 297  
Qy 246 SAASR-----HSES----- 254  
Db 298 QSLKRSARKYGRGHFWTTSMKPSAEQMQDHSSSDSNMNNDAASLENSASDEEDI 357  
Qy 255 ---PRKSSILVSLRTHNN-----SSITAFKV----- 278  
Db 358 GSETRAIYSIVLKPGHSTILNSTKLPSQDWLQVPEBELGTVDLERKASKLQAOQSMDDG 417  
Qy 279 GSFWR-----ESAA-----LRQ 291  
Db 418 GSFQKSPSKLPIDQESAVDTAKASDVSSVGTATATPLSPKCATLAKRFALKTRSQITK 477  
Qy 292 REYAEILGRGLASLAILLSAPALCMAPYCLFTIYLVSTYPRTERPKSVWYSIAFWLQMF 351  
Db 478 RKMSLIKAKAQTLSAILAFITITWTPYINMVLV-NTFDCSCIPKTYW-NLGWVLCYI 535  
Qy 352 NSFVNPFLYPLCHRRFQKAFWKIL 375  
Db 536 NSTVNPVCYALCNKTFRTTFMILL 559

RESULT 6  
 151837  
 muscarinic receptor - rat  
 C/Species: Rattus sp. (rat)  
 C/Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 24-Nov-1999  
 C/Accession: 151837  
 R/Ref: J. J. Smith, T. L. Mei, L. J. Ikeda, M. J. Fujiwara, Y. J. Gomez, J. J. Halonen, M. J. Roeske  
 Adv. Exp. Med. Biol. 287, 313-330, 1991  
 A/Title: The molecular properties of the M1 muscarinic receptor and its regulation of cy  
 A/Reference number: 151837; PMID:92101806; PMID:11759615  
 A/Accession: 151837  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-460 <RES>  
 A/Cross-references: GB:S73971; NID:g241253; PIDM:AAB20705.1; PID:g241254  
 C/Genetics:  
 A/Gene: m1  
 C/Superfamily: vertebrate rhodopsin

Query Match 20.0%; Score 410; DB 2; Length 460;  
 Best Local Similarity 27.4%; Pred. No. 1,8e-27;  
 Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;

QY 5 NSTGILPPAAQVPLAFL--MSFPAFAIMVGNVLAFAVDRNLRRHSNYFFLNLALSD 61  
 Db 12 NITVLAPEGKPMQVAFIGITGTLSTLVGNLLVLSFKVNTLKTNNVYFLSLACAD 71  
 QY 62 FLVGLSIPLYIHVLF-MNRFSGICMFWLIDYLLCTASVYNIIVISIDRYQSVNAV 120  
 Db 72 LIIGTSMNLTYTYLLMGHALGTACDMLADLYASNSVNNLLISFDRFESVTRPL 131  
 QY 121 SYRAQHTGIMKIYVAVVAV-VILAFLVNGPMILASDSKNSVTNK-----DCEPGFVTEW 174  
 Db 132 SYRAKRT--PRRAALMIGLAMIVSFVMAPAIL---FMQYLVGERVTLAQCYIQFLSQP 166  
 QY 175 YILITTMLEFLLPVISAVFNVQIYWSLMK-----RAL-----SRCPSHAFSTSSS 224  
 Db 187 IITFGTMAAFYLPVTVMC---TLVYRIYRETNRRARBELAALQGSSTPKGGSSSSSE 242  
 QY 225 AS-----GHLHRAVACRT-----SNPGLKESASRSSESRRK 258  
 Db 243 RSQPGAGSPSPSPGRCCR---CCRAPRLLQAVSWKEEEDGESLTSSECEP--G 297  
 QY 259 SSILVSL-----RTHNNSITAFKVGSPFMRSESA-----ALRQREY 294  
 Db 298 SEVVIMKPMVDSBAQAPTKQPPKSPNTVAKPTKKG---RDRGKGQKPRGKQLAKRKT 354  
 QY 295 AELLRGKRLARSLAIIISAFALCMAPYCLFTYVLSYPTERPKSVWYSIAFWLQWNSF 354  
 Db 355 FSLVKEKKAARTLSAIIALFILTPTPYNIMVLV-STFCDCVPEITLW-ELGYWLCVYNST 412  
 QY 355 VNPFLYPLCHRRFOKAFWKILCVTKW 380  
 Db 413 VNPWCYALCNKAFRDTF-RLLILCRW 437

RESULT 7  
 A29514  
 muscarinic acetylcholine receptor M1 - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
 C/Accession: A94518; A94293; A37121; A29514  
 R/Bonner, T. J.  
 submitted to Genbank, July 1987  
 A/Reference number: A94518  
 A/Accession: A94518  
 A/Molecule type: mRNA  
 A/Residues: 1-460 <BO2>  
 A/Cross-references: UNIPROT:P08482  
 R/Bonner, T. J.; Buckley, N. J.; Young, A. C.; Brann, M. R.  
 Science 237, 527-532, 1987  
 A/Title: Identification of a family of muscarinic acetylcholine receptor genes.

A/Reference number: A94293; PMID:87263421; PMID:3037705  
 A/Accession: A94293  
 A/Molecule type: mRNA  
 A/Residues: 1-227/338-460 <BO2>  
 A/Experimental source: cerebellar cortex  
 A/Note: only a part of the protein translation is given; none of the nucleotide sequence  
 J. Kurtenbach, E. J. Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.  
 R. Biol. Chem. 265, 13702-13708, 1990  
 A/Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invo  
 A/Reference number: A37121; PMID:90337982; PMID:2280182  
 A/Accession: A37121  
 A/Status: preliminary  
 A/Molecule type: Protein  
 A/Residues: 62-124 <KUR>  
 C/Superfamily: vertebrate rhodopsin  
 C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
 F/25-50/Domain: transmembrane #status predicted <TM1>  
 F/62-93/Domain: transmembrane #status predicted <TM2>  
 F/100-121/Domain: transmembrane #status predicted <TM3>  
 F/142-168/Domain: transmembrane #status predicted <TM4>  
 F/187-209/Domain: transmembrane #status predicted <TM5>  
 F/367-387/Domain: transmembrane #status predicted <TM6>  
 F/402-420/Domain: transmembrane #status predicted <TM7>  
 F/212/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 20.0%; Score 410; DB 2; Length 460;  
 Best Local Similarity 27.4%; Pred. No. 1,8e-27;  
 Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;

QY 5 NSTGILPPAAQVPLAFL--MSFPAFAIMVGNVLAFAVDRNLRRHSNYFFLNLALSD 61  
 Db 12 NITVLAPEGKPMQVAFIGITGTLSTLVGNLLVLSFKVNTLKTNNVYFLSLACAD 71  
 QY 62 FLVGLSIPLYIHVLF-MNRFSGICMFWLIDYLLCTASVYNIIVISIDRYQSVNAV 120  
 Db 72 LIIGTSMNLTYTYLLMGHALGTACDMLADLYASNSVNNLLISFDRFESVTRPL 131  
 QY 121 SYRAQHTGIMKIYVAVVAV-VILAFLVNGPMILASDSKNSVTNK-----DCEPGFVTEW 174  
 Db 132 SYRAKRT--PRRAALMIGLAMIVSFVMAPAIL---FMQYLVGERVTLAQCYIQFLSQP 166  
 QY 175 YILITTMLEFLLPVISAVFNVQIYWSLMK-----RAL-----SRCPSHAFSTSSS 224  
 Db 187 IITFGTMAAFYLPVTVMC---TLVYRIYRETNRRARBELAALQGSSTPKGGSSSSSE 242  
 QY 225 AS-----GHLHRAVACRT-----SNPGLKESASRSSESRRK 258  
 Db 243 RSQPGAGSPSPSPGRCCR---CCRAPRLLQAVSWKEEEDGESLTSSECEP--G 297  
 QY 259 SSILVSL-----RTHNNSITAFKVGSPFMRSESA-----ALRQREY 294  
 Db 298 SEVVIMKPMVDSBAQAPTKQPPKSPNTVAKPTKKG---RDRGKGQKPRGKQLAKRKT 354  
 QY 295 AELLRGKRLARSLAIIISAFALCMAPYCLFTYVLSYPTERPKSVWYSIAFWLQWNSF 354  
 Db 355 FSLVKEKKAARTLSAIIALFILTPTPYNIMVLV-STFCDCVPEITLW-ELGYWLCVYNST 412  
 QY 355 VNPFLYPLCHRRFOKAFWKILCVTKW 380  
 Db 413 VNPWCYALCNKAFRDTF-RLLILCRW 437

RESULT 8  
 S47572  
 muscarinic acetylcholine receptor m3 - bovine  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 09-Jul-2004  
 C/Accession: S47572  
 R/Lee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K. J.  
 Biochim. Biophys. Acta 1223, 151-154, 1994  
 A/Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 re  
 A/Reference number: S47572; PMID:94339178; PMID:8061048  
 A/Accession: S47572

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-590 <LEEA-  
A:Cross-references: UNIPROT:P41984; EMBL:U08286; NID:g520465; PIDD:AAA51866.1; PID:g5204  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: neurotransmitter receptor

Query Match 20.0%; Score 409.5; DB 2; Length 590;  
Best Local Similarity 25.0%; Pred. No. 2.6e-27;  
Matches 126; Conservative 83; Mismatches 134; Indels 161; Gaps 17;

18 LAFMSSFAFAIMGNVAVILAFVVDRLRHSNYFFLNLASDPLVGLISIPYIPVL 77  
Db 71 IAFGLVLAIVTIIGNLIIVVAFKVNKQKTVNNFFLLSLACADLIIGVISNMLFTTYII 130  
Qy 78 FN-WNFGSGICFWLITDYLLCTASVYNIIVLSYDRYQSVNASTYRAOHT---GIMKI 132  
Db 131 MNRMLGNLACDLMISIDYVNASVNMVLVISFDRYSITRPLTYRAKRTTKRAGWIG 190  
Qy 133 VAQWAVVILAFVNGPMILASDSWKNSTNTDCERG---FVTEWYLLITTMLEFL 187  
Db 191 LA-----WISFILAAPAL--FWOYEVGKRTVPGECEFIQFLSEPTTFGTATAATYM 242  
Qy 188 PVISVAVNVOIYWSLWKRRALSRCPSHAGF--STTSSASGHLRAGVACRTSNPLKE 245  
Db 243 PVTIMTI---LYWRIYKETE-KRTKELAGLQASGTEAEAFVHPVPTGSSRSCSYELQ 297  
Qy 246 SAASR-----HSES----- 254  
Db 298 QSMKSAARKYGRCHFWFTTKSKWPSAEQMDQDHSDDSNMNNDAASLENSASDEEDI 357  
Qy 255 ---PRKSSIVSLFTH---NMS-----STAFKV----- 278  
Db 358 GSETTAIYISVAKLGHSTILNTYLPSNDLQVEEBELGSLERKPSKLTQOQMDG 417  
Qy 279 GSFNRS-----ESAA----- 291  
Db 418 GSFQSFSLQPLESADVTAKASDVNSVGKTATPLPLSFKEATLAKRPAKTRSQITK 477  
Qy 292 REYAEELGRKLAISLAILLSAFAICWAPYCLFTVLTSTYPTERTPKSVWSTIAFWLQMF 351  
Db 478 RKMSLIEKKAQAQTLAAILLAFITWTPYNIWLV-NTFCDSCIPTYW-NLGYWLCYI 535  
Qy 352 NSFNPFLYPCRRFOKAFMKIL 375  
Db 536 NSTVNPVCYALCNKTRFTFKML 559

# RESULT 9

A29476 muscarinic acetylcholine receptor M4 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C:Accession: A29476  
R:Braun, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.  
Biochem. Res. Commun. 149, 125-132, 1987  
A:Title: A novel subfamily of muscarinic receptor identified by homology screening.  
A:Reference number: A29476; MUID:88077068; PMID:3120722  
A:Accession: A29476  
A:Molecule type: mRNA  
A:Residues: 1-589 <BRNA  
A:Cross-references: UNIPROT:P08483; GB:M18088; NID:g202657; PIDD:AAA40659.1; PID:g202658  
A:Experimental source: brain  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme  
F:67-90/Domain: transmembrane #status predicted <TM1>  
F:104-124/Domain: transmembrane #status predicted <TM2>  
F:142-163/Domain: transmembrane #status predicted <TM3>  
F:184-206/Domain: transmembrane #status predicted <TM4>  
F:230-251/Domain: transmembrane #status predicted <TM5>  
F:493-512/Domain: transmembrane #status predicted <TM6>  
F:527-545/Domain: transmembrane #status predicted <TM7>

Query Match 19.7%; Score 403; DB 2; Length 589;  
Best Local Similarity 23.8%; Pred. No. 9.3e-27;  
Matches 125; Conservative 84; Mismatches 145; Indels 172; Gaps 15;

4 SNSTGILPMAO-----VPLAFMSSFAFAIMGNVAVILAFVVDRLRHSNYFFLNLAS 58  
Db 51 SNTSDSLGGHTIQQVVFIAFLTGLFALVTIIGNLIIVVAFKVNKQKTVNNFFLLSLA 110  
Qy 59 ISDFVLGLISIPYIPYHLEN-WNFGSGICFWLITDYLLCTASVYNIIVLSYDRYQSVS 117  
Db 111 CADLIIGVISNMLFTTYIIMNRMLGNLACDLMISIDYVNASVNMVLVISFDRYSIT 170  
Qy 118 NAVSYRAOHT---GIMKIIVQWAVVILAFVNGPMILASDSWKNSTNTDCERG--- 169  
Db 171 RPLTYRAKRTTKRAGWIGLA-----WISFILAAPAL--FWOYEVGKRTVPGECEFI 222  
Qy 170 -FVTEWYLLITTMLEFLLPVISVAVNVOIYWSLWKRRALSRCPSHAGF--STTSSAS 226  
Db 223 QFLSEPTTFGTALAAAFVPTIMTI---LYWRIYKETE-KRTKELAGLQASGTEAEAE 277  
Qy 227 GHLRAGVACRTSNPLKESASRSESPPRK----- 258  
Db 278 NFVHPTGSSRSCSYELQOQGVKR---SSRRYGRCHFWFTTKSKWPSAEQMDQDHSDD 334  
Qy 259 -----SSILVSLRTHMNSI----- 273  
Db 335 SMNNDAASLENSASDEEDIGSETTAIYISVAKLGHSTILNTYLPSNDLQVEEBELG 394  
Qy 274 -----TAFKVGSEFMRSESA----- 288  
Db 395 LGTVDERNAHKLQAKSMGDNQOQDFTLPIQLSADVDTGKTSNDTSSADKTATLPL 454  
Qy 289 -----LRQYAEELGRKLAISLAILLSAFAICWAPYCLFTVLTSTYPTERTPKSV 329  
Db 455 LSFKEATLAKRPAKTRSQITRKRMSLIEKKAQAQTLAAILLAFITWTPYNIWLV-N 513  
Qy 330 TYPTERTPKSVWSTIAFWLQMFNSFVNPLPLCHRRFOKAFMKIL 375  
Db 514 TFRDSCIPTYW-NLGYWLCYINSTVNPVCYALCNKTRFTFKML 559

# RESULT 10

S10128 muscarinic acetylcholine receptor M4 - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C:Accession: S10128  
R:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramchandran, J.; Capon, D.J  
EMBO J. 6, 3923-3929, 1987  
A:Title: Distinct primary structures, ligand-binding properties and tissue-specific exp  
A:Reference number: S04326; MUID:8816632; PMID:3443095  
A:Accession: S10128  
A:Molecule type: DNA  
A:Residues: 1-590 <PER>  
A:Cross-references: UNIPROT:P20309; EMBL:X15266; NID:g32323; PIDD:CAA33337.1; PID:g32324  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme  
F:68-95/Domain: transmembrane #status predicted <TM1>  
F:105-131/Domain: transmembrane #status predicted <TM2>  
F:143-164/Domain: transmembrane #status predicted <TM3>  
F:184-207/Domain: transmembrane #status predicted <TM4>  
F:231-252/Domain: transmembrane #status predicted <TM5>  
F:493-513/Domain: transmembrane #status predicted <TM6>  
F:525-546/Domain: transmembrane #status predicted <TM7>  
F:5,6,15,41/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.7%; Score 402.5; DB 2; Length 590;  
Best Local Similarity 24.0%; Pred. No. 1e-26;  
Matches 121; Conservative 86; Mismatches 135; Indels 163; Gaps 16;

18 LAFMSSFAFAIMGNVAVILAFVVDRLRHSNYFFLNLASDPLVGLISIPYIPYHVL 77  
Db 71 IAFGLVLAIVTIIGNLIIVVAFKVNKQKTVNNFFLLSLACADLIIGVISNMLFTTYII 130



QY 78 FN-WNFGSGICMFWLITDYLCTASVYNIVLISYDRQSVSNVYRAOHT---GIMKI 132  
 Db 131 MNRWALGNLACDLWLAIIDYASNSVNNLVISFDRFFSTRPLTYAKKTRKAGMIG 190  
 QY 133 VAQWAVWILAFVNGMILASDSWKNSTNTKCEPG---FVTEWYILITMLLEPLL 187  
 Db 191 LA-----WVISFVLMARAIL---FWQYFVGKRTVPPECEFIQFLSEPTITFGTAAAFM 242  
 QY 188 PVISVAVFNQIYWSLWK----- 205  
 Db 243 PVITIMTI---LWRIYKETEKRTELKELAGLQASGTEAFENFVHPGSSSSCYELOQQ 298  
 QY 206 -----RRALSRCPSHAGFSTT-----SSSAGHLRAGVACRTSNPGKES 246  
 Db 299 SMKRSNRRKYGRC--HWFTTKSWKPSSEQMDQDHSSSDSMNNNDAAALSNASSED 356  
 QY 247 AAGR-----HS----- 252  
 Db 357 IGSETRAIYSIVLKLPGHSTILNSTKLPSDDLQVPEELGMVDLERKADKLQAKSVD 416  
 QY 253 --ESPRAKSIIVSLR-----THNNSI-----TAFKVS-----FMSSESAALR 290  
 Db 417 GGSFPPKSFSLPQLQESAVDTAKTSDVNSSVGKSTATLPLSFKEATLAKRPALKTRSOIT 476  
 QY 291 QREYAEILRGKRLARSLAIIILSAFALCMAPYCLFTIYSTYPTREPKSVWYSIAFWLQW 350  
 Db 477 KRRBMSLVKEXKAQOTLSAILLAFIITWTPYINIMVLV-NFCDSCIPKTFW-NLGWVLCY 534  
 QY 351 FNSFVNPFLYPLCHRRPQKAFWKIL 375  
 Db 535 INSTVNPVCYALCNKTFRTTFKML 559

RESULT 11  
 B29514  
 muscarinic acetylcholine receptor M3 - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text\_change 09-Jul-2004  
 C/Accession: B94518; B94293; B37121; B29514  
 R/Bonner, T.I.  
 submitted to GenBank, July 1987  
 A/Reference number: A94518  
 A/Accession: B94518  
 A/Molecule type: mRNA  
 A/Residues: 1-589 <B01>  
 A/Cross-references: UNIPROT:P08483  
 R/Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.  
 Science 237, 527-532, 1987  
 A/Title: Identification of a family of muscarinic acetylcholine receptor genes.  
 A/Reference number: A94293; MUID:87263421; PMID:3037705  
 A/Accession: B94293  
 A/Molecule type: mRNA  
 A/Residues: 1-269/463-589 <B02>  
 A/Experimental source: cerebral cortex  
 A/Note: only a part of the protein translation is given; none of the nucleotide sequence  
 R/Kurtenbach, E.; Cuttler, C.A.M.; Pedder, E.K.; Altken, A.; Harris, A.C.M.; Hulme, E.C.  
 J. Biol. Chem. 265, 13702-13708, 1990  
 A/Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues inv  
 A/Reference number: A37121; MUID:90337982; PMID:2380182  
 A/Accession: B37121  
 A/Molecule type: protein  
 A/Residues: 104-166 <KUR>  
 C/Superfamily: vertebrate rhodopsin  
 C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme  
 F/67-90/Domain: transmembrane #status predicted <TM1>  
 F/104-124/Domain: transmembrane #status predicted <TM2>  
 F/142-163/Domain: transmembrane #status predicted <TM3>  
 F/184-206/Domain: transmembrane #status predicted <TM4>  
 F/230-251/Domain: transmembrane #status predicted <TM5>  
 F/492-512/Domain: transmembrane #status predicted <TM6>  
 F/527-545/Domain: transmembrane #status predicted <TM7>

F/6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 19.6%; Score 402; DB 2; Length 589;  
 Best local similarity 23.8%; Pred. No. 1,1e-26;  
 Matches 125; Conservative 84; Mismatches 145; Indels 172; Gaps 15;

QY 4 SNSTGILPPAAQ-----VPLAFMSSFAFAIMVGAAVVIAFYVDNRNLRHSNYFLNLTA 58  
 Db 51 SNTSDSLPGHITMQLQVVFIAFLTGLALVTIIGNILVIAFVKNQKLTQVNNYFLLSLA 110  
 QY 59 ISDFVLGLSIPYIYHVLFN-WNFGSGICMFWLITDYLCTASVYNIVLISYDRQSVS 117  
 Db 111 CADLIIGVISMNLFTYITINRWALGNLACDLWLSDYASNSVNNLVISFDRYFSIT 170  
 QY 118 NAVSYRAOHT---GIMKIYAVWVILAFVNGMILASDSWKNSTNTKCEPG--- 169  
 Db 171 RPLTYAKKTRKRGWIGLA-----WVISFVLMARAIL---FWQYFVGKRTVPPECFI 222  
 QY 170 -FVTEWYILITMLLEPLLPVISVAVFNQIYWSLKKRRLSRCPHAGF--STSSAS 226  
 Db 223 OFLSEPTITFGTAAAFVNPVITMTI---LWRIYKETE-KRTELKELAGLQASGTEAEAE 277  
 QY 227 GHHRAGVACRTSNPGKESASRHSSEPRK----- 258  
 Db 278 NFVHPGSSRSCSSYELQOGVVR---SSRKYGCHFWFTKSWKPSABQMDQDHSSSD 334  
 QY 259 -----SSILSRTHNNSI----- 273  
 Db 335 SMNNNDAAALSNASSEDIDGSETRAIYSIVLKLPGHSTILNSTKLPSDDLQVSNED 394  
 QY 274 -----TAFKVSFWRSSESA----- 288  
 Db 395 LGTVDERNAHKLQAKSMGDNQKDFTKLPQLQESAVDTAKTSDTNSAKKTATLPL 454  
 QY 289 -----LQREYAEILRGKRLARSLAIIILSAFALCMAPYCLFTIYVS 329  
 Db 455 LSFKEATLAKRPALKTRSOITTKRKRMSLKERKAAQOTLSAILLAFIITWTPYINIMVLV-N 513  
 QY 330 TYPTREPKSVWYSIAFWLQWNSFVNPFLYPLCHRRPQKAFWKIL 375  
 Db 514 TPCDSCIPKTFW-NLGWVLCYINSTVNPVCYALCNKTFRTTFKTL 558

RESULT 12  
 A55019  
 muscarinic acetylcholine receptor, M3 isoform - chicken  
 C/Species: Gallus gallus (chicken)  
 C/Date: 11-Nov-1994 #sequence revision 11-Nov-1994 #text\_change 09-Jul-2004  
 C/Accession: A55019  
 R/Gadbut, A.P.; Galper, J.B.  
 J. Biol. Chem. 269, 25823-25829, 1994  
 A/Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and  
 A/Reference number: A55019; MUID:95014393; PMID:7929287  
 A/Accession: A55019  
 A/Molecule type: mRNA  
 A/Status: preliminary  
 A/Residues: 1-639 <GAD>  
 A/Cross-references: UNIPROT:P49578; GB:L10617; NID:9530097; PION:AAA65961.1; PID:9530098  
 C/Superfamily: vertebrate rhodopsin  
 C/Keywords: neurotransmitter receptor

Query Match 19.6%; Score 401; DB 2; Length 639;  
 Best local similarity 24.4%; Pred. No. 1,5e-26;  
 Matches 124; Conservative 84; Mismatches 136; Indels 164; Gaps 16;

QY 16 VPLAFMSSFAFAIMVGAAVVIAFYVDNRNLRHSNYFLNLASDFVLGLSIPYIYH 75  
 Db 117 VPLAFMSSFAFAIMVGAAVVIAFYVDNRNLRHSNYFLNLASDFVLGLSIPYIYH 176  
 QY 76 VLF-MNFGSGICMFWLITDYLCTASVYNIVLISYDRQSVSNVYRAOHT---GIM 130  
 Db 177 IIVGHALGNLACDLWLSDYASNSVNNLVISFDRYFSITRPLTYAKKTRKAGVM 236



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Oy 131 KIVAQWVAWIIAFLVNGPMLIASDSW-----KNSNTKDCPCGFTEWYILITMLLEF 185
Db 237 IGLA-----WISFLMAPAIL---FWQYFVKRIVPDECIQGLSEIITFGAIAIAF 288
Oy 186 LLPVISAIVFVNOIYWSIMKRRLSRCPSHAGFSTTSSA--SGHLRAGVACRTSNPGL 243
Db 289 YLPVIMSI-----LYWRIYKETE-KRTKELAGLQASGSEAFARFVHQGSSRSLSVEL 343
Oy 244 KESASRHSSESPRRS----- 259
Db 344 QROSTKRSRRKRRKCHFWLTWKSWEPTDQGDQSHSSDSWNNDAAASLENSASDDE 403
Oy 260 -----SILVELRTH-----MNSSTIAPKV----- 278
Db 404 DITAEITAIYISIVLCPGHSALINSTKLPSSSEDLNESADELQSDTDOEKPKLQEPK 463
Oy 279 -----GSFWR-----ESAL----- 289
Db 464 SIODGSGFQSKPLPIQPSAETATASDGSSVTKTSAALPLSPKREATLAKKPAKTRRS 523
Oy 290 --RQREYELLRGRKLASLAILLSAPALCMAPYCLFTIYVSTYRTERPKSVWISIAFW 347
Db 524 QITKREKSLIKKKAQTLISALIFAFTITWTPYINMVLV-NTFCDV-PTKTV-NLGYW 580
Oy 348 LQWENSFVNPFLYPLCHRRFOKAFWKIL 375
Db 581 LCTINSTVNPVCYALCNKCMFRFTFQML 608

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RESULT 13

```

A:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 24-Nov-1999
C:Accession: A31897
R:Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.
J. Biol. Chem. 263, 18397-18403, 1988
A:Title: Isolation, sequence, and functional expression of the mouse M1 muscarinic acetylcholine receptor.
A:Reference number: A52694; MUID:89054021; PMID:2848036
A:Accession: A31897
A:Molecule type: DNA
A:Residues: 1-460 <SHA>
R:Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.
J. Biol. Chem. 264, 6596, 1989
A:Reference number: A52742
A:Contents: annotation; erratum, correct translation of residue 119
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
F:25-50/Domain: transmembrane #status predicted <TM1>
F:62-93/Domain: transmembrane #status predicted <TM2>
F:100-121/Domain: transmembrane #status predicted <TM3>
F:142-168/Domain: transmembrane #status predicted <TM4>
F:187-209/Domain: transmembrane #status predicted <TM5>
F:367-387/Domain: transmembrane #status predicted <TM6>
F:402-420/Domain: transmembrane #status predicted <TM7>

```

```

Query Match 19.5%; Score 400; DB 2; Length 460;
Best Local Similarity 27.0%; Pred. No. 1.3e-26;
Matches 120; Conservative 86; Mismatches 152; Indels 86; Gaps 19;
Oy 5 NSTGLPRAQVPLAFLMSS---FAFALMGNAVITLAFVYDRNRHSNPFPLNLASD 61
Db 12 NITVALPQKPMQVAFISTTGLSLATVGNLVLISIKVTEKTKTNNPFLSLACAD 71
Oy 62 FLVGLISIPLYPIHPLF-NMNGSGICMFWLTITDYLCTASVYINVLISYRQSVSNV 120
Db 72 LIIGFSSNVLYTITLMMGMALGTIACDLMLADLVASNASVMNLLISFPRYEVTPPL 131
Oy 121 SYRAQHTGIMKIIVAQWVAW-IIAFLVNGPMLIASDSKNSNTNK-----DCEPGFTW 174
Db 132 SYRAKRT--PRRAALMIGLAWLSFVLWAPAIL---FWQYLVGERTVLACGCIQIFLSQP 186

```

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Oy 175 YILITMLLEFLPVISVAVFNOIYWSIMKR-----RAL-----SRCPSHAGFSTSSS 224
Db 187 IITGTAMAAAYLPTWNC-----ITYWRIYETENRARELAAQSEIFPGKGGSSSSSE 242
Oy 225 AS-----GHILRAGVACT-----SNPGIKESAASRHSSESPRRK 258
Db 243 RSQGAEGSPSPGRCR-----CCRAPLLQAYSWKEEBEEDGSMELTSSSEGEFP--G 297
Oy 259 SSILVSL-----RTMNSITAFK-----VGSFWRSESAALRQREYAE 296
Db 298 SEVIAKPMWVDEAQAFTKQPPKSPNTKPKTKKGRDGKQKQKPKRKEQNAKRTPS- 356
Oy 297 LLRGRKLARSLAILLSAPALCMAPYCLFTIYVSTYRTERPKSVWISIAFWLQWNSFVN 356
Db 357 LVKKAARITSAIILAFILITWTPYINMVLV-SIFCKDCEVETLM-ELGYLCLVNSITVN 414
Oy 357 PFLYPLCHRRFOKAFWKILCVTKW 380
Db 415 PMCYASCNKAFRDHF-RLLLCRW 437

```

RESULT 14

```

A:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
C:Accession: J05530
R:Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.
Neuron 1, 403-410, 1988
A:Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor.
A:Reference number: J05530; MUID:90166521; PMID:3272174
A:Accession: J05530
A:Molecule type: DNA
A:Residues: 1-532 <BON>
C:Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neurotransmitter acetylcholine.
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
F:30-53/Domain: transmembrane #status predicted <TM1>
F:67-87/Domain: transmembrane #status predicted <TM2>
F:105-126/Domain: transmembrane #status predicted <TM3>
F:147-169/Domain: transmembrane #status predicted <TM4>
F:192-214/Domain: transmembrane #status predicted <TM5>
F:444-464/Domain: transmembrane #status predicted <TM6>
F:479-498/Domain: transmembrane #status predicted <TM7>
F:8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

```

Query Match 19.5%; Score 399.5; DB 2; Length 532;
Best Local Similarity 24.6%; Pred. No. 1.7e-26;
Matches 122; Conservative 90; Mismatches 142; Indels 141; Gaps 15;
Oy 16 VPLAFLMSSPFAFALMGNAVITLAFVYDRNRHSNPFPLNLASDPLVGLISIPLYPH 75
Db 31 ITIAVAVAVSLITIVGVVLMISFKVNSQKLTNNYLLSLACADLISGFSSNMLYTTY 90
Oy 76 VLF-NMNGSGICMFWLTITDYLCTASVYINVLISYRQSVSNVSYRAQHT-----GIM 130
Db 91 ILMGRMALGSLACDLMLADLVASNASVMNLLISFDRYFSTPLTYRAKRTPKRAGIM 150
Oy 131 KIVAQWVAWIIAFLVNGPMLIASDSW-----KNSNTKDCPCGFTEWYILITMLLEF 185
Db 151 IGLA-----WISFLMAPAILC---WQYLVGKRTVPLDECIQIFLSPTITFGAIAIAF 202
Oy 186 LLPVISAIVFVNOIYWSIMKR----- 213
Db 203 YIPVSWTILYCRIVRETERKTKDLAQSDSVTKAEKRPAPARALFRSCLRCRPTLA 262
Oy 214 -----SHAGFTT---SSASGHLRAG-----VACRT-----SNPGLK 244
Db 263 QREKQASWSSSSRSRSTSTTGKPSQATGPSANMAAEOULTTSSIPSSDEDEKPAIDPVLQ 322
Oy 245 ESAASRHSSESPRRKSLIVSLRTMNSI--TAKVGSFWRSESAALR----- 290
Db 323 VVYSQGESFGEFSAABETETFYKABTEKSDVDTNPVLLSPAAAHPRKQKCAVAKFR 382

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QY 291 -----OREVAELRGRLAR 305
DB 383 LVVKADNGNRTNNGCHKVIMPCFPVAKKEPSTKGLNPNPNSHQMTKRRKRVLVKERKAAQ 442
QY 306 SLAILLSAPFICWAPYCLFTIVLSTYPTREPKSWYSIAFWLQWNSFVNPFYPLCHR 365
DB 443 TLSAILLAFTITWTPYIMVLV-STFCDKCVPTLMH-LGYWLCYVSTVNPICYALCNR 500
QY 366 RFQKAFWKILCVTKM 380
DB 501 TFRKTF-KMLLCRW 514
```

## RESULT 15

```
S71323
alpha-1A adrenergic receptor - Japanese medaka
C:Species: Oryzias latipes (Japanese medaka)
C:Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
C:Accession: S71323
R:Yasuno, A.; Abe, K.; Arai, S.; Emori, Y.
Eur. J. Biochem. 235, 501-507, 1996
A:Title: Molecular cloning and functional expression of the alpha-1A-adrenoceptor of Me
A:Reference number: S71323; MUID:96184522; PMID:8654394
A:Accession: S71323
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-477 <YAS>
A:Cross-references: EMBL:D63859
A>Note: It is uncertain whether Met-1 or Met-8 is the initiator
C:Superfamily: vertebrate rhodopsin
```

Query Match 19.24; Score 392.5; DB 2; Length 477;

Best Local Similarity 28.04; Pred. No. 5.9e-26;

Matches 115; Conservative 65; Mismatches 145; Indels 85; Gaps 15;

```
QY 4 SNGSTGILP-----AAQVPLAFLMSSFAFMWGNVILAFVVDRLRHSNYFFLNLAI 59
DB 18 SNGSHVLAPELNTVKAVLGMVLGIFILFGVIGNIIVLISVCHRHQTVTYFYIVNLAV 77
QY 60 SDPLVGLISIFL-YIPHVLFNNNFGSGICMFWLITDYLLCTASVYNIVLISYDRQSVSN 118
DB 78 ADLLLSSTVLPFSAIFELIDRWVFGVFCNIMAAVDVLCCTASIMSLCVISVDKYGVSX 137
QY 119 AVSIRAQHTGIMKIYAQMVAWIIAFLVN-GPMILASDSWKNSTNTKD--C---EPGFV 171
DB 138 PLKYPALMTGRRLIAVML-LWVLVSIIIGPLF---GKKEPAPEDETVCITTEPGYA 192
QY 172 TEWYIITITMLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFTTSSASGHLHR 231
DB 193 -----IFSAVGSFYPLALIIILMYCRV----- 215
QY 232 AGVACTSNGGLKESASRSSEPRKSSILVSLRTMNSITAFKVGSEFRSESAALRQ 291
DB 216 --VVAQKESRGLKEGQKIEKSDSEQ-----VILRMHNGNTTV-----SEDEALRS 258
QY 292 REVAEL-----LGRKRLASLAILLSAFACWAPYCLFTIVLSTYPTREPKSWYSIAF 346
DB 259 KTFPALRLKFSREKKAATLGIVGCFVLCMLPFFVLPIGSIFF-AYRPSDTVFKITF 317
QY 347 WLQWFNSFVNPFYPLCHRRFOKAFWKIL--CVTKMPA-----LSQNGS 388
DB 318 WLGYFNSCIPITTYLCSNGEKKAFQSLGVHCLRMTPRAHHHLISVGQS 367
```

Search completed: April 6, 2005, 19:33:31  
job time : 29 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 16:57:52 ; Search time 85 Seconds  
(without alignments)  
2355.564 Million cell updates/sec

Title: US-10-626-445-8  
Perfect score: 2048  
Sequence: 1 MSENSTGILPPAQAQVPLAF.....WKILCVTKWPAISQNSVSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2035	99.4	391	2	Q91ZY2
2	1745	85.2	391	2	Q91ZY1
3	1372.5	67.0	390	2	Q96LD9
4	1370.5	66.9	390	1	HHAR_HUMAN
5	1311.5	64.0	390	1	Q8WNV9
6	1238	60.4	389	2	Q91ZY3
7	722.5	35.3	445	1	HHAR_HUMAN
8	721	35.2	445	1	HHAR_CAVPO
9	718.5	35.1	445	2	Q865E1
10	718.5	35.0	445	1	HHAR_RAT
11	715.5	34.9	445	1	HHAR_MOUSE
12	704.5	34.4	473	2	Q6ZM33
13	665.5	32.5	365	2	Q8WY01
14	665.5	32.5	373	2	Q8WY29
15	547	26.7	174	2	Q6U9U4
16	543	26.5	175	2	Q6U9J5
17	492.5	24.0	301	2	Q8WY00
18	492.5	24.0	309	2	Q8WY00
19	418	20.4	460	1	ACM1_MACMU
20	415.5	20.3	530	2	Q8VH24
21	414.5	20.2	532	1	ACMS_MACMU
22	413	20.2	454	1	Q66RH1
23	413	20.2	460	1	ACM1_HUMAN
24	413	20.2	460	1	ACM1_PIG
25	410.5	20.0	531	1	ACMS_RAT
26	410.5	20.0	531	1	ACMS_PIG
27	410	20.0	460	1	ACM1_PAT
28	410	20.0	587	2	Q8VH26
29	409.5	20.0	590	2	ACM3_BOVIN
30	408	19.9	585	1	ACM3_CAEEL
31	406.5	19.8	532	2	Q81VW0

32	406	19.8	490	2	Q7T286
33	405.5	19.8	200	2	Q8N150
34	405	19.8	458	2	Q8VH28
35	404.5	19.8	532	1	ACMS_HUMAN
36	404	19.7	589	1	ACM3_MOUSE
37	403.5	19.7	590	1	ACM3_PONPY
38	402.5	19.7	564	2	Q96RG9
39	402.5	19.7	590	1	ACM3_GORGO
40	402.5	19.7	590	1	ACM3_HUMAN
41	402.5	19.7	590	1	ACM3_PANTR
42	402	19.6	589	1	ACM3_RAT
43	401.5	19.6	528	2	Q9PTF6
44	401.5	19.6	532	2	Q920H4
45	401	19.6	460	1	ACM1_MOUSE

## ALIGNMENTS

RESULT 1	Q91ZY2	PRELIMINARY	PRT	391 AA.
AC	Q91ZY2			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Histamine H4 receptor.			
GN	Name=Hrh4;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
NCBI	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c;			
RA	Liu C., Wilson S., Kuel C., Lovenberg T.W.;			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).			
CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
DR	EMBL; AF358859; AAK97380.1; -.			
DR	MGD; MGI:2429635; Hrh4.			
DR	GO; GO:0005615; C:extracellular space; TAS.			
DR	GO; GO:0005887; C:integral to plasma membrane; IC.			
DR	GO; GO:0005624; C:membrane fraction; IDA.			
DR	GO; GO:0004969; F:histamine receptor activity; IDA.			
DR	GO; GO:0006954; P:inflammatory response; TAS.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHDOPRN.			
DR	PRINTS; PR01726; HISTAMINEH4R.			
DR	PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.			
DR	PROSITE; PS0262; G_PROTEIN_RECPT_F2_1; 1.			
KW	G-protein coupled receptor; Receptor; Transmembrane.			
KW	SEQUENCE 391 AA; 44248 MW; 59EC73CB5214C5E0 CRC64;			
Query Match	99.4%	Score 2035;	DB 2;	Length 391;
Best Local Similarity	99.7%	Pred. No. 1.2e-125;		
Matches 390;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MSENSTGILPPAQAQVPLAF	MSFAIMVGNVILAFVVDRLRRRSNYFFLNLAI	60
DB	1	MSENSTGILPPAQAQVPLAF	MSFAIMVGNVILAFVVDRLRRRSNYFFLNLAI	60
QY	61	DFVLGLISPIYIPHVLFNNFGSICFMFLITDYLLCTASVYIVLISYDRQSVSNV		120
DB	61	DFVLGLISPIYIPHVLFNNFGSICFMFLITDYLLCTASVYIVLISYDRQSVSNV		120
QY	121	SYRQHTGIMKIVQMVVILAFVNGPMLIASQWNSNTNOCCEGPTWETILT		180
DB	121	SYRQHTGIMKIVQMVVILAFVNGPMLIASQWNSNTNOCCEGPTWETILT		180
QY	181	MLLEFLPVISVAVFNVQIYWSLWKRRALSRCPHAGSTTSSASGHLHRGAVACRTSN		240
DB	181	MLLEFLPVISVAVFNVQIYWSLWKRRALSRCPHAGSTTSSASGHLHRGAVACRTSN		240

QY 241 PGKESASRHSSEPRKSSILVSLRTHNNSITAFVGSFWRSESAALRQREYAEILRG 300  
DB 241 PGKESASRHSSEPRKSSILVSLRTHNNSITAFVGSFWRSESAALRQREYAEILRG 300  
QY 301 RKLARSIALILSAFAICWAPYCLFTYVLSYPTTERPKSVWYSIAFWLQWNSFVNDPLY 360  
DB 301 RKLARSIALILSAFAICWAPYCLFTYVLSYPTTERPKSVWYSIAFWLQWNSFVNDPLY 360  
QY 361 PLCHRRFOKAFWKILCVTKMPALSONOSVSS 391  
DB 361 PLCHRRFOKAFWKILCVTKMPALSONOSVSS 391

## RESULT 2

ID 0912Y1 PRELIMINARY; PRT; 391 AA.  
AC 0912Y1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Histamine H4 receptor  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RA Liu C., Wilson S., Kueh C., Lovenberg T.W.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL: AF358860; AA97381.1; C: integral to membrane; IEA.  
DR GO: GO:0016021; C: integral to membrane; IEA.  
DR GO: GO:0004872; F: receptor activity; IEA.  
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.  
DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . ; IEA.  
DR Pfam: PF00001; 7tm.1; 1.  
DR PRINTS: PR00237; GPCRHOOPS.  
DR PROSITE: PR01726; HISTAMINEH4.  
DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 391 AA; 44023 MW; C707BA639CFED41 CRC64;

Query Match 85.2%; Score 1745; DB 2; Length 391;  
Best Local Similarity 84.9%; Pred. No. 1.2e-106;  
Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;

QY 1 MSESNGTGILPPAAQVPLAFMSFAFAIWNVAIVTLAFVVDNRNLHRNSYFFNLAIIS 60  
DB 1 MSESNGTDVPLRPAQVPLAFMSFAFAITGNVAVTLAFVADNRNLHRNSYFFNLAIIS 60  
QY 61 DPLVGLISIPLYIPHLFENNFGSGICMFWLITDYLLCTASVYNIIVLISYDRQSVNAV 120  
DB 61 DPLVGVISIPLYIPHLFENNFGSGICMFWLITDYLLCTASVYNIIVLISYDRQSVNAV 120  
QY 121 SYRAQHTGIMKIYAQWVAWVILAFVNGPMILASDSMKNSTNTKDCPEGFTEWYILIT 180  
DB 121 SYRAQHTGIMKIYAQWVAWVILAFVNGPMILASDSMKNSTNTKDCPEGFTEWYILIT 180  
QY 121 RYRAQHTGIMKIYAQWVAWVILAFVNGPMILASDSMKNSTNTKDCPEGFTEWYILIT 180  
DB 121 RYRAQHTGIMKIYAQWVAWVILAFVNGPMILASDSMKNSTNTKDCPEGFTEWYILIT 180  
QY 181 MLEFLLPVIVSAVFNVOIYMSLMKRALSRCPHAGFSTTSSASGHLRAGVACRTSN 240  
DB 181 MLEFLLPVIVSAVFNVOIYMSLMKRALSRCPHAGFSTTSSASGHLRAGVACRTSN 240  
QY 241 PGKESASRHSSEPRKSSILVSLRTHNNSITAFVGSFWRSESAALRQREYAEILRG 300  
DB 241 PGKESASRHSSEPRKSSILVSLRTHNNSITAFVGSFWRSESAALRQREYAEILRG 300  
QY 301 RKLARSIALILSAFAICWAPYCLFTYVLSYPTTERPKSVWYSIAFWLQWNSFVNDPLY 360  
DB 301 RKLARSIALILSAFAICWAPYCLFTYVLSYPTTERPKSVWYSIAFWLQWNSFVNDPLY 360

QY 361 PLCHRRFOKAFWKILCVTKMPALSONOSVSS 391  
DB 361 PLCHRRFOKAFWKILCVTKMPALSONOSVSS 391

## RESULT 3

ID 096LD9 PRELIMINARY; PRT; 390 AA.  
AC 096LD9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Histamine receptor H4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=21106319; Pubmed=11179435;  
RA Nguyen T., Shapiro D.A., George S.R., Setola V., Lee D.K., Cheng R.,  
RA Kauter L., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;  
RT "Discovery of a novel member of the histamine receptor family.";  
RL Mol. Pharmacol. 59:427-433(2001).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL: AY008280; AL09297.1; C: integral to membrane; IEA.  
DR GO: GO:0016021; C: integral to membrane; IEA.  
DR GO: GO:0004872; F: receptor activity; IEA.  
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.  
DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . ; IEA.  
DR InterPro: IPR000276; GPCR\_Rhodopsin.  
DR InterPro: IPR008102; HistamineRecept\_H4.  
DR Pfam: PF00001; 7tm.1; 1.  
DR PRINTS: PR00237; GPCRHOOPS.  
DR PRINTS: PR01726; HISTAMINEH4.  
DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 390 AA; 44469 MW; CC82B5D30D16C66 CRC64;

Query Match 67.0%; Score 1372.5; DB 2; Length 390;  
Best Local Similarity 68.1%; Pred. No. 3e-82;  
Matches 267; Conservative 41; Mismatches 81; Indels 3; Gaps 2;

QY 1 MSESNGTGILPPAAQVPLAFMSFAFAIWNVAIVTLAFVVDNRNLHRNSYFFNLAIIS 60  
DB 1 MADTNSITINISLSTRVTLAFPMELVAFALMGALVILAFVVDKNLHRNSYFFNLAIIS 60  
QY 61 DPLVGLISIPLYIPHLFENNFGSGICMFWLITDYLLCTASVYNIIVLISYDRQSVNAV 120  
DB 61 DPLVGVISIPLYIPHLFENNFGSGICMFWLITDYLLCTASVYNIIVLISYDRQSVNAV 120  
QY 121 SYRAQHTGIMKIYAQWVAWVILAFVNGPMILASDSMKNSTNTKDCPEGFTEWYILIT 180  
DB 121 SYRAQHTGIMKIYAQWVAWVILAFVNGPMILASDSMKNSTNTKDCPEGFTEWYILIT 180  
QY 121 SYRAQHTGIMKIYAQWVAWVILAFVNGPMILASDSMKNSTNTKDCPEGFTEWYILIT 180  
DB 121 SYRAQHTGIMKIYAQWVAWVILAFVNGPMILASDSMKNSTNTKDCPEGFTEWYILIT 180  
QY 181 MLEFLLPVIVSAVFNVOIYMSLMKRALSRCPHAGFSTTSSASGHLRAGVACRTSN 240  
DB 179 SFLEFIPVIVSAVFNVOIYMSLMKRALSRCPHAGFSTTSSASGHLRAGVACRTSN 240  
QY 241 PGKESASRHSSEPRKSSILVSLRTHNNSITAFVGSFWRSESAALRQREYAEILRG 300  
DB 239 SASTEPASRHSSEPRKSSILVSLRTHNNSITAFVGSFWRSESAALRQREYAEILRG 238  
QY 301 RKLARSIALILSAFAICWAPYCLFTYVLSYPTTERPKSVWYSIAFWLQWNSFVNDPLY 360  
DB 299 RKLARSIALILSAFAICWAPYCLFTYVLSYPTTERPKSVWYSIAFWLQWNSFVNDPLY 358  
QY 361 PLCHRRFOKAFWKILCVTKMPALSONOSVSS 391  
DB 359 PLCHRRFOKAFWKILCVTKMPALSONOSVSS 390

RESULT 4  
 HH4R HUMAN STANDARD; PRT; 390 AA.  
 AC OGH3N8; OGG200;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Histamine H4 receptor (HH4R) (GPRV53) (G protein-coupled receptor 105)  
 DE (GPCR105) (SP1144) (AXOR35).  
 GN Name=HH4;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2053417; PubMed=10973974; DOI=10.1074/jbc.M006480200;  
 RA Oda T., Morikawa N., Saito Y., Matsuho Y., Matsumoto S.-I.;  
 RT "Molecular cloning and characterization of a novel type of histamine  
 RT receptor preferentially expressed in leukocytes.";  
 RL J. Biol. Chem. 275:36781-36786(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC TISSUE=Leukocyte;  
 RX MEDLINE=20568725; PubMed=1118334; DOI=10.1006/bbrc.2000.4008;  
 RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;  
 RT "Molecular cloning and characterization of a new human histamine  
 RT receptor, HH4R.";  
 RL Biochem. Biophys. Res. Commun. 279:615-620(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Jones P.G., Wu S., Betsy M.;  
 RT "Cloning of a novel histamine receptor.";  
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC TISSUE=Bone marrow;  
 RX PubMed=11179434;  
 RA Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofstra C.L., Blevitt J.,  
 RA Pyatt J., Li X., Chai W., Carruthers N., Lovenberg T.W.;  
 RT "Cloning and pharmacological characterization of a fourth histamine  
 RT receptor (H4) expressed in bone marrow.";  
 RL Mol. Pharmacol. 59:420-426(2001).  
 RN [5]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC TISSUE=Eosinophil;  
 RX MEDLINE=21104636; PubMed=1181941;  
 RA Morse K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A.,  
 RA Antnes J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N.,  
 RA Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M.,  
 RA Monsema P.J. Jr.;  
 RT "Cloning and characterization of a novel human histamine receptor.";  
 RL J. Pharmacol. Exp. Ther. 296:1058-1066(2001).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21106320; PubMed=11179436;  
 RA Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dycko G.M., Mannan I.J.,  
 RA Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L.,  
 RA Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S.,  
 RA Bergsma D.J., Fitzgerald L.R.;  
 RT "Cloning, expression, and pharmacological characterization of a novel  
 RT human histamine receptor.";  
 RL Mol. Pharmacol. 59:434-441(2001).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA O'Reilly M.A.;  
 RT "Identification of a histamine H4 receptor on human eosinophils - Role  
 RT in eosinophil chemotaxis.";  
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.  
 RN [8]  
 RP SEQUENCE FROM N.A.

RA Puhl H.J., Iikeda S.R., Aronstam R.S.;  
 RT "cDNA clones of human proteins involved in signal transduction  
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
 RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: The H4 subclass of histamine receptors could mediate the  
 CC histamine signals in peripheral tissues. Displays a significant  
 CC level of constitutive activity (spontaneous activity in the  
 CC absence of agonist).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed primarily in the bone marrow and  
 CC eosinophils. Shows preferential distribution in cells of  
 CC immunological relevance such as T-cells, dendritic cells,  
 CC monocytes, mast cells, neutrophils. Also expressed in a wide  
 CC variety of peripheral tissues, including the heart, kidney, liver,  
 CC lung, pancreas, skeletal muscle, prostate, small intestine,  
 CC spleen, fetal liver and lymph node.  
 CC -1- INDUCTION: Expression is either up-regulated or down-regulated  
 CC upon activation of the lymphoid tissues and this regulation may  
 CC depend on the presence of IL-10 or IL-13.  
 CC -1- MISCELLANEOUS: Does not bind diphenhydramine, lorazepam,  
 CC ranitidine, cimetidine and chlorpheniramine. Shows modest affinity  
 CC for dimaprit, impromidine, clobenpropit, thiopeperamide, burinamide  
 CC clobenpropit, impromidine and imetit. The order of inhibitory activity  
 CC was imetit > clobenpropit > burinamide > thiopeperamide.  
 CC Clobenpropit behaves as a partial agonist, dimaprit and  
 CC impromidine show some agonist activity while clobenpropit behaves as  
 CC a full agonist. Thiopeperamide shows inverse agonism (enhances cAMP  
 CC activity). The order of inhibitory activity of histamine  
 CC derivatives was Histamine > N-alpha-methylhistamine > R(-)-alpha-  
 CC methylhistamine > S(+)-alpha-methylhistamine. Both N-alpha-  
 CC methylhistamine > R(-)-alpha-methylhistamine behave as full  
 CC agonists.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; AB044934; BAB13698.1; -  
 CC EMBL; AB045370; BAB30091.1; -  
 CC EMBL; AF307973; AAG32052.1; -  
 CC EMBL; AF312230; AAK12081.1; -  
 CC EMBL; AF329449; AAK43542.1; -  
 CC EMBL; AF325356; AAL01684.1; -  
 CC EMBL; AJ298292; CAC83493.1; -  
 CC EMBL; AY136745; AAN01271.1; -  
 CC PIR; J07366; J07566.  
 CC GeneW; HGNC:17383; HRH4.  
 CC MIM; 606792; -  
 CC GO; GO:0016021; C:Integral to membrane; NAS.  
 CC GO; GO:0004969; F:histamine receptor activity; NAS.  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC InterPro; IPR008102; HistamineRecept\_H4.  
 CC Pfam; PF00001; 7tm\_1; 1.  
 CC PRINTS; PR00237; GPCRHOPOPSN.  
 CC PRINTS; PR01726; HISTAMINEHR4.  
 CC PROSITE; PS00237; G\_PROTEIN\_RECPT\_F1\_2; 1.  
 CC PROSITE; PS50262; G\_PROTEIN\_RECPT\_F1\_2; 1.  
 CC G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;  
 CC Transmembrane.  
 CC DOMAIN 1 19  
 CC TRANSMEM 20 40 Extracellular (Potential).  
 CC DOMAIN 41 52 1 (Potential).  
 CC TRANSMEM 53 73 Cytoplasmic (Potential).  
 CC DOMAIN 74 87 2 (Potential).  
 CC TRANSMEM 88 108 Extracellular (Potential).  
 CC DOMAIN 109 131 3 (Potential).  
 CC TRANSMEM 132 152 Cytoplasmic (Potential).  
 CC DOMAIN 153 172 4 (Potential).  
 CC TRANSMEM 172 172 Extracellular (Potential).  
 CC DOMAIN 153 172

FT TRANSMEM 173 193 5 (Potential).  
 FT DOMAIN 194 304 Cytoplasmic (Potential).  
 FT TRANSMEM 305 325 6 (Potential).  
 FT DOMAIN 326 341 Extracellular (Potential).  
 FT TRANSMEM 342 362 7 (Potential).  
 FT DOMAIN 363 390 Cytoplasmic (Potential).  
 FT DISULFID 87 164 By similarity.  
 FT CARBOHYD 5 5 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 9 9 N-linked (GlcNAc. . .) (Potential).  
 FT LIPID 374 374 S-palmitoyl cysteine (Potential).  
 FT CONFLICT 138 138 A -> V (in Ref. 1).  
 FT CONFLICT 206 206 H -> R (in Ref. 1).  
 FT CONFLICT 253 253 Q -> R (in Ref. 1).  
 SQ SEQUENCE 390 AA; 44495 MW; C98658AE7FF912C3 CRC64;

Query Match 66.9%; Score 1370.5; DB 1; Length 390;  
 Best Local Similarity 68.1%; Pred. No. 4,1e-82;  
 Matches 26; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSNSTGTGLPPAAQVPLAFMSSFAFAINAVNVLAFVVDNLRHRSNYFFLNLAIS 60  
 DB 1 MPDNTSTINLSSTRVTLAFMSLVAFIMLGNALVILAFVVDKLNLRHRSYFFLNLAIS 60  
 QY 61 DELVGLISIPLYIPHLFNNNGSGICMFWLITDYLLCTASVNIIVLISYDRYOSVSN 120  
 DB 61 DFEVGVISIPLYIPHLFNNNGSGICMFWLITDYLLCTASVNIIVLISYDRYOSVSN 120  
 QY 121 SYAHOHTGIMKIYAQWAVWILAFVNGPMILASDSMNSTNTKDCBPFTVTEYILIT 180  
 DB 121 SYTOHTGVKIYTLTAVAVWILAFVNGPMILVSESKDEGS--ECBPFGSEWYILAIT 178  
 QY 181 MLLEFLPVISVAFVNOIYWSLWKRRALSCPSHAGFTSTSSASGHLRHAGVACRTSN 240  
 DB 179 SFLEFVYPIVLLVAFVNNIYWSLWKRRDHLSCQSHPELTAVSSNTICGHSFRGLSSRSL 238  
 QY 241 PGLKESASRHSPPRRKSSILVSLRTHNMSITAFVNGSFMSBSAALRQRYAEILRG 300  
 DB 239 SASTEPVASHSRQRKSSLMFSSRTKWNSTIASMGSPQSDSVALLQRSHVELLRA 298  
 QY 301 RKLARSALILLSAFALCMAPCYCFTLYLSTYPTERPKSVWYSIAFWLQWNSFVNPFL 360  
 DB 299 RKLAKSLAILLGFAVCMAPYSILFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPFL 358  
 QY 361 PLCHRRFQKAFWKILCVTKMPALSO--NQSVSS 391  
 DB 359 PLCHRRFQKAFWKILCVTKMPALSO--NQSVSS 390

RESULT 5  
 Q8WNV9 PRELIMINARY; PRT; 390 AA.  
 AC Q8WNV9;  
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)  
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
 DE Histamine H4 receptor.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sui.  
 NCBI\_TaxID=9823;  
 RN NCBI\_TaxID=9823;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22015261; PubMed=12020829; DOI=10.1016/S0167-4781(02)00236-1;  
 RA Oda T., Matsunoto S., Maezono Y., Takaueki J., Matsunoto M.,  
 RA Kamohara M., Saito T., Onishi T., Soga T., Hiyaama H., Matsushime H.,  
 RA Furutachi K.;  
 RT "CDNA cloning and characterization of porcine histamine H4 receptor";  
 RL Biochim. Biophys. Acta 1575:135-138(2002).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL: AB053300; BAB83078.1; -;  
 DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0004872; F:receptor activity; IEA.  
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHOPOPSN.  
 DR PRINTS: PR01726; HISTAMINEHAR.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 390 AA; 44483 MW; BC8FD363A6F4AD3F CRC64;

Query Match 64.0%; Score 1311.5; DB 2; Length 390;  
 Best Local Similarity 65.9%; Pred. No. 3e-78;  
 Matches 259; Conservative 33; Mismatches 96; Indels 5; Gaps 3;

QY 1 MSBSN--STGILPPAAQVPLAFMSSFAFAINAVNVLAFVVDNLRHRSNYFFLNLA 58  
 DB 1 MSAINNTNTNLTPLNTRIALAFMSLALVIMGNVILAFVVDKLNLRHRSNYFFLNLA 60  
 QY 59 ISDFVGLISIPLYIPHLFNNNGSGICMFWLITDYLLCTASVNIIVLISYDRYOSVSN 118  
 DB 61 ISDFVGVISIPLYIPHLFNNNGSGICMFWLITDYLLCTASVNIIVLISYDRYOSVSN 120  
 QY 119 ASYRAQHTGIMKIYAQWAVWILAFVNGPMILASDSMNSTNTKDCBPFTVTEYILIT 178  
 DB 121 ASYRTOHTGILKIYAVWILAFVNGPMILASDSMNSTNTKDCBPFTVTEYILIT 178  
 QY 179 ITMLLEFLPVISVAFVNOIYWSLWKRRALSCPSHAGFTSTSSASGHLRHAGVACRTSN 238  
 DB 179 ITLFFELPVLVAFVNNIYWSLWKRRHLSRQSHCELTIVSSQWGHSPFCGLPSST 238  
 QY 239 SNGLKESASRHSPPRRKSSILVSLRTHNMSITAFVNGSFMSBSAALRQRYAEIL 298  
 DB 239 SLSDPREAASLHSEPRRKSSTLWFLSTR--SLTASKKGFLSHSDSLALQKHEILL 297  
 QY 299 RGLKARSALILLSAFALCMAPCYCFTLYLSTYPTERPKSVWYSIAFWLQWNSFVNPFL 358  
 DB 298 RKLAKSLAILLGFAVCMAPYSILFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPFL 357  
 QY 359 LVPCHRRFQKAFWKILCVTKMPALSONOSVSS 391  
 DB 358 LVPCHRRFQKAFWKILCVTKMPALSONOSVSS 390

RESULT 6  
 Q91ZY3 PRELIMINARY; PRT; 389 AA.  
 AC Q91ZY3;  
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
 DE Histamine H4 receptor.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.  
 NCBI\_TaxID=10141;  
 RN NCBI\_TaxID=10141;  
 RP SEQUENCE FROM N.A.  
 RA Liu C., Wilson S., Xuei C., Lovenberg T.W.;  
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL: AF358858; AK97379.1; -;  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHOPOPSN.  
 DR PRINTS: PR01726; HISTAMINEHAR.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 389 AA; 4451 MW; 51A3Z2FD6FC1C3E4F CRC64;

Query Match 60.4%; Score 1238; DB 2; Length 389;  
Best Local Similarity 62.5%; Pred. No. 2e-73;  
Matches 245; Conservative 43; Mismatches 100; Indels 4; Gaps 3

OY 1 MEESNTGTLPPAAQVPLAFWMSFAFWMGAAVVITLAFVDNRILRHNSNPFNLTAIS 60  
| : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : |  
DB 1 MANNST-IATSIKISTLTFLMSLLAIAMGLGNVVVLAFIDRNLRHSNYFFNLATA 59  
OY 61 DFLVGLISIPLYTIPHFLFMNFSGSCMFMLIDYLLCASVYNIVLISDYRQSVNAV 120  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 60 DPFVGALIAFLPIRSSLLTYTSKOACVMRLIDYLCLTRASYNIIVLISDIKIOSVANV 119  
OY 121 SYRAOHTGMKIWAQVAVVILAFLVNGPMILASDSMNSTNKDCEPGFTVEWTLLTT 180  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 120 WYRAQHSIGMKIATQGVAVVIFSPMNGPILISDSMQNST--EEEPFLKKMYFALT 177  
OY 181 MLLEFLLPVISAAYFNVOIYWSLMKRALSRCPSHAGF-STISSASGLHLRAGA CRTS 239  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 178 SLLEFLIPILLVAFYFAHIYWSIMKEKLSRCLSHLVLDSDSSSDHGHCSDPDPSRAT 237  
OY 240 NGDLKSASRSSESPRKSSITVSLRTMTNSSITAFKGSFMRSESAALROREYAE LR 299  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 238 LPARKETTSLSGDSKRKSSLFSTRAYKNVSIVASKGFLSHSSLSALOHEHELPR 297  
OY 300 GRKLARSLAILSAFICAWPYCLPTIVLSTYPRTERPKSWYSIAFWLOWENSFVNPL 359  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 298 AKRLAKSLAILDAFPAICWAPSLTVVIISPFPERNLSTSYHTNAFWLQWNFSFVNPL 357  
OY 360 YPLCHRRFOKAFWKILCTWKMPALSONOVSS 391  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 358 YPLCHRRFOKAFLKILPVRRGSTPPPHNRIS IST 389

RESULT 7

H3R\_HUMAN  
ID H3R\_HUMAN STANDARD; PRT; 445 AA.  
AC Q9YSN1; O9GX22; O9H4K8;  
DT 28-FEB-2003 (Rel. 41, Created)  
DD 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Histamine H3 receptor (H3R) (G protein-coupled receptor 97).  
GN Name=HRH3; Synonyms=GPCR97;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxId=9606;  
RN [1]  
RX RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Thalamus;  
RX MEDLINE=99278519; PubMed=10347254;  
RX LOVENBERG T.W., Roland B.L., Wilson S.J., Jiang X., Pyatt J.,  
RA Huverberg T.W., Jackson M.R., Erlender W.G.;  
RT "Cloning and functional expression of the human histamine H3  
receptor.";  
RT Mol. Pharmacol. 55:1101-1107(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.  
RX MEDLINE=20569125; PubMed=1118334; DOI=10.1006/dbic.2000.4008,  
RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;  
RT "Molecular cloning and characterization of a new human histamine  
receptor, HRH4.";  
RT Biochem. Biophys. Res. Commun. 279:615-620(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1, 3, 4, 5, 6 AND 7).  
RC TISSUE=Thalamus;  
RX MEDLINE=21181559; PubMed=11284713; DOI=10.1042/0264-6021.3550279;  
RA Cogge F., Guenot S.-P., Audinot V., Renourdet-Try A., Beauvanger P.,  
RA Macia C., Ouvry C., Nagel N., Righe H., Boutin J.A., Galluzzi J.-P.;  
RT "Genomic organization and characterization of splice variants of the  
human histamine H3 receptor.";  
RT Biochem. J. 355:279-288(2001).

[4]  
SEQUENCE FROM N.A. (ISOPFORM 1), AND VARIANT SHY-DRAGER SYNDROME  
VAL-280.  
TISSUE=Blood;  
MEDLINE=21953333; PubMed=11956964; DOI=10.1007/s007020200036;  
Wiedemann P., Boenisch H., Oertere F., Brues M.,  
"Structure of the human histamine H3 receptor gene (HRH3) and  
identification of naturally occurring variations",  
J. Neural Transm. 109:443-453(2002).  
[5]  
SEQUENCE FROM N.A. (ISOPFORM 3).  
Ullmer C., Zirres E., Lubbert H.,  
"Cloning and functional expression of the human histamine H3S  
receptor",  
Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.  
[6]  
SEQUENCE FROM N.A. (ISOPFORM 1).  
MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggaley C.L.,  
Bailey J.P., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,  
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cordy N.R.,  
Coulson A., Coville G.J., Deodhar R., Dhani P.D., Dunn M.,  
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
Lahvesaaho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
Marsh V.L., Martin S.L., McConachie I.J., McLeay K., McMurray A.A.,  
Meline S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
Oliver K., Parter A., Patel R., Pearce T.A.V., Peck A.I.,  
Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,  
Rice C.M., Ross M.T., Scott C.B., Senra H.K., Showkhen R., Sims S.,  
Skuse C.D., Smyth M.L., Soderlund C., Steward C.A., Suleston J.E.,  
Swann R.M., Swamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
Tracey A., Tromane A.C., Vaudin M., Wall M., Wallis J.M.,  
Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
Willing L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
Rogers J.,  
"The DNA sequence and comparative analysis of human chromosome 20.",  
Nature 414:865-871(2001).  
[7]  
FUNCTION: The H3 subclases of histamine receptors could mediate the  
histamine signals in CNS and peripheral nervous system. Signals  
through the inhibition of adenylyl cyclase and displays high  
constitutive activity (spontaneous activity in the absence of  
agonist). Agonist stimulation of isoform 3 neither modified  
adenylyl cyclase activity nor induced intracellular calcium  
mobilization.  
[8]  
SUBCELLULAR LOCATION: Integral membrane protein.  
[9]  
ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=7;  
Comment=Additional isoforms seem to exist;  
Name=1;  
IsoId=Q9YSN1-1; Sequence=Displayed;  
Name=2;  
IsoId=Q9YSN1-2; Sequence=VSP\_001886;  
Name=3; Synonyms=H3S;  
IsoId=Q9YSN1-3; Sequence=VSP\_001885;  
Name=4;  
IsoId=Q9YSN1-4; Sequence=VSP\_001881;  
Name=5;  
IsoId=Q9YSN1-5; Sequence=VSP\_001882;  
Name=6;  
IsoId=Q9YSN1-6; Sequence=VSP\_001883;  
Name=7;  
IsoId=Q9YSN1-7; Sequence=VSP\_001884;  
[10]  
TISSUE SPECIFICITY: Expressed predominantly in the CNS, with the  
greatest expression in the thalamus and caudate nucleus. The  
various isoforms are mainly coexpressed in brain, but their



CC	relative expression level varies in a region-specific manner.	
CC	isoforms 3 and 7 are highly expressed in the thalamus, caudate	
CC	nucleus and cerebellum while isoforms 5 and 6 show a poor	
CC	expression. Isoforms 5 and 6 show a high expression in the	
CC	amygdala, substantia nigra, cerebral cortex and hypothalamus.	
CC	Isoform 7 is not found in hypothalamus or substantia nigra.	
CC	-1- DISEASE: Defects in HRH3 are a cause of Shy-Drager syndrome	
CC	(MIM:146500). This syndrome is characterized by orthostatic	
CC	hypotension, bladder and bowel incontinence, anhidrosis, iris	
CC	atrophy, amyotrophy, ataxia, rigidity and tremor.	
CC	-1- MSCLEAFOUS: Does not bind to cimetidine and triptolidine. Shows	
CC	modest affinity for thoperamide, melleit, N-alpha-methylhistamine	
CC	and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to	
CC	iodopropyfan while isoforms 1 and 3 bind it with high affinity.	
CC	-1- SMILIRAF: Belongs to the G-protein coupled receptor 1 family.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch">http://www.isb-sib.ch/announce/</a>	
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
CC	-----	
DR	EMBL, AF140538; AAD31815.1; -	
DR	EMBL, AB045369; BAB20090.1; -	
DR	EMBL, AB019000; BAB17030.1; -	
DR	EMBL, AJ296652; CAC51025.1; -	
DR	EMBL, AJ278250; CAC39434.1; -	
DR	EMBL, AL078633; CAC04014.1; -	
DR	EMBL, AF363791; AAK50040.1; -	
DR	Genew; HGNC:5184; HRH3.	
DR	MIM; 604525; -	
DR	MIM; 146500; -	
DR	GO; GO:0005887; C:Integral to plasma membrane; TAS.	
DR	GO; GO:0004969; F:histamine receptor activity; TAS.	
DR	GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.	
DR	GO; GO:0007289; P:neurotransmitter secretion; TAS.	
DR	InterPro; IPR000276; GPCR_Rhodopsn.	
DR	InterPro; IPR003980; H3_receptor.	
DR	Pfam; PF00001; 7tm.1; 1-	
DR	PRINTS; PR00237; GPCRHRHODPSN.	
DR	PRINTS; PR01471; HISTAMINEHR3.	
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.	
DR	PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.	
KW	Alternative splicing; Disease mutation; G-protein coupled receptor;	
KW	Glycoprotein; Transmembrane.	
FT	DOMAIN	1
FT	TRANSMEM	40
FT	TRANSMEM	61
FT	TRANSMEM	71
FT	TRANSMEM	92
FT	TRANSMEM	109
FT	TRANSMEM	130
FT	TRANSMEM	157
FT	TRANSMEM	178
FT	TRANSMEM	197
FT	TRANSMEM	218
FT	TRANSMEM	360
FT	TRANSMEM	381
FT	TRANSMEM	396
FT	TRANSMEM	417
FT	TRANSMEM	445
FT	TRANSMEM	20
FT	TRANSMEM	250
FT	TRANSMEM	292
FT	TRANSMEM	298
FT	TRANSMEM	11
FT	TRANSMEM	85
FT	TRANSMEM	98
FT	TRANSMEM	197
FT	TRANSMEM	315
FT	TRANSMEM	227
FT	TRANSMEM	342
FT	TRANSMEM	234
FT	TRANSMEM	263

FT	VASPPLIC	274	353		/FtId=VSP_001864.
FT	VASPPLIC	445	445		Missing (In isoform 3).
FT	VASPPPLC	445	445		/FtId=VSP_001865.
FT	VARIANT	280	280		K -> KKKKKTCTL (in isoform 2).
FT	VARIANT	280	280		/FtId=VSP_001866.
FT	VARIANT	280	280		A -> V (in Shy-Dragger syndrome).
FT	CONFLICT	19	19		/FtId=VAR_012335.
FT	SEQUENCE	445 AA;	48671 MW;		E -> D (in Ref. 1 and 5).
QY	Match				2ACFT440FB59B6C CRC64;
Query Match					
Best Local Similarity		35.3%;	Score 722.5;	DB 1;	Length 445;
Matches 165;	Conservative 51;	Mismatches 116;	Indels 93;	Gaps 10;	
OY	18	LAFIMSEFAFMIGNAVIIPVVDNRRLHRSNYFFFLNALISDFVLGISPIYIPHYL	77		
Dd	37	LAALMALILIVATVGNALVMIAFPADSSLRQNPFLLNLISDFLVGAPFCIPLYVPYL	96		
OY	78	F-ANNPFGSGICMFLINDYLLCTASVYNIVLISDRYGVSNAVSYPRAOHGMKVIAQM	136		
Dd	97	TGRMTFPGGLCKMLVNDYLLCTSSAFETVLISYDRFLSVRAVSYPRAOQDTPRAVKM	156		
OY	137	VAWVILAFLVNGPMILASDSWK-----NSTTKXCEPEGFTEWYILITTMLEFLLPYIS	191		
Dd	157	LLVVWLAFLLXGPAIL---SWEYLSGGSSIIEGHGYAEFFNWVFLIRASTLTFFPTPLS	213		
OY	192	VAYRNVQIY-----WSIKRKALSRCSH	215		
Dd	214	VTFFNLSIYINLIQRTRRLLDGEAAAGPEPPPAQPSPPPPQCWCQKQHGAEMPLH	273		
OY	216	-----AQSFTTSSASGHLIRAGVACTSNGLKESASARSESPPRRKSILV	263		
Dd	274	RVGVEAAVGAAGAEATLGGGGGG---GSVASPTSSG---SSSRTERPR-----	318		
OY	264	SLRTNMNSITRAFVSGFWRESASAALROR-----EYAEILRGRLARSIALILSAF	314		
Dd	319	-----SLRGSFKPSASSSLEKRMAMVQSFRQLRLSDRKVAASLVIYSIF	367		
OY	315	AICMAPYCLFTIVLISTYPRTERPKSVWSIAFWLQWFNSFYNPPLYPCRRPOKAFWKI	374		
Dd	368	GLCWAPYTLMIITIPAACHGCVP--DYWEYTSFMTLMANSAVNPLYPLCHHSFRAPFTKL	426		
OY	375	LCVTK	379		
Dd	427	LCPOK	431		
<b>RESULT 8</b>					
HHR3_CAVPO	STANDARD,	PRT;	445 AA.		
ID_HHR3_CAVPO	09J135; 09J136;				
AC	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Histamine H3 receptor (HHR3).				
DN	Name=HHR3;				
OS	Cavia porcellus (Guinea pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.				
OX	NCBT_TaxID=10141;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).				
RP	TISSUE=Brain;				
RC	MEDLINE=20218440; PubMed=10757514;				
RX	Tardivel-Jacombe J., Rouleau A., Heron A., Morisset S., Pillot C.,				
RA	Cochois V., Schwartz J.-C., Arrang J.-M.,				
RT	"Cloning and cerebral expression of the guinea pig histamine H3				
RL	receptor: evidence for two isoforms."				
CC	NeuroReport 11:755-759(2000).				
CC	-I- FUNCTION: The H3 subclass of histamine receptors could mediate the				
CC	histamine signals in CNS and peripheral nervous system. Signals				
CC	through the inhibition of adenylylate cyclase and displays high				
CC	constitutive activity (spontaneous activity in the absence of				

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CC CC      agonist).
CC CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC CC      -1- ALTERNATIVE PRODUCTS:
CC CC      Event-Alternative splicing; Named isoforms=2;
CC CC      Name=Long; Synonym=H3L;
CC CC      IsoId=Q9J13-1; Sequence=Displayed;
CC CC      Name=Short; Synonym=H3S;
CC CC      IsoId=Q9J13-2; Sequence=VSP_001880;
CC CC      -1- TISSUE SPECIFICITY: Expressed widely and abundantly throughout the
CC CC      brain. Highly expressed in discrete neuronal populations such as
CC CC      pyramidal cells in cerebral cortex or cerebellar Purkinje cells.
CC CC      -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC      between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC      or send an email to license@isb-sib.ch).
CC CC      -----
DR DR      EMBL; AF267537; AAF78947.1; -.
DR DR      EMBL; AF267538; AAF78950.1; -.
DR DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR DR      InterPro; IPR003980; H3_receptor.
DR DR      Pfam; PF00001; 7tm.1; 1.
DR DR      PRINTS; PR00237; GPCR_RHODOPSIN.
DR DR      PRINTS; PR01471; HISTAMINEH3R.
DR DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR DR      PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW KW      Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW KW      Transmembrane.
FT FT      DOMAIN 1 40 Extracellular (Potential).
FT FT      TRANSMEM 41 61 Potential.
FT FT      DOMAIN 62 71 Cytoplasmic (Potential).
FT FT      TRANSMEM 72 92 Potential.
FT FT      DOMAIN 93 109 Extracellular (Potential).
FT FT      TRANSMEM 110 130 Potential.
FT FT      DOMAIN 131 157 Cytoplasmic (Potential).
FT FT      TRANSMEM 158 178 Potential.
FT FT      DOMAIN 179 197 Extracellular (Potential).
FT FT      TRANSMEM 198 218 Potential.
FT FT      DOMAIN 219 359 Cytoplasmic (Potential).
FT FT      TRANSMEM 360 380 Potential.
FT FT      DOMAIN 381 398 Extracellular (Potential).
FT FT      TRANSMEM 399 419 Potential.
FT FT      DOMAIN 420 445 Cytoplasmic (Potential).
FT FT      CARBOHYD 11 24 Poly-Ala.
FT FT      VARSPLIC 276 305 N-linked (GlcNAc...) (Potential).
FT FT      Missing (in isoform Short).
SQ SQ      SEQUENCE 445 AA; 48734 MW; BAE206A3887189A0 CRC64;
Query Match 35.2%; Score 721; DB 1; Length 445;
Best Local Similarity 39.8%; Pred. No. 1,7e-39;
Matches 162; Conservative 54; Mismatches 133; Indels 58; Gaps 9;
QY 18 LAFLMSFAFIMGNVAVIIAFVVDRLRHSNYFFLNLASDFVLGLISIPLYIPHYL 77
DB 38 LAALMALIIVATVGNALVMLAFVADSLRQNNFFLNLAIISDFVGFICPLVYPVYL 97
QY 78 F-ANNFGSGICMFILITDYLLCTASVYNIIVLISYDRYOSVSNVSYRAOHGIMKIVAQ 136
DB 98 TGRWTFGRGLCKMLVVDYLLCTSSVFNIVLISYDRFVSVTRAAYSRAOQSDTRAAVRKM 157
QY 137 VAVVILAFVNGPMILASDSMK-----NSTWTKDCEPFVTEWYILITITMLLEFLLPYIS 191
DB 158 VLVVVLALVLYGPAL---SWEYLSGSSIPBGHCYAFEFYNNWYLLTASTLEFPTPLS 214
QY 192 VAVFNVQY-----WSLWKRRALSRCPS 214
DB 215 VTFPNLSIYLNIOQRTRLRLDGAAREAGPDLPEAQSPPPPPCGCMGCMQGGQESMPL 274

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QY 215 HA-GPSTTSSA-SGHLRAGVACRTSNPGLKESASRHSSEPRRKSILVLRTHMNS 272
DB 275 HRYGVGAQPGARAEALAGCGSGAASPSTSSSSSSTGERP-----SLKGSKRS 327
QY 273 ITAFVGSFPMWSESALRQREYAEILRGRKLARSIALILSAFACWAPCYLFTVLYSTP 332
DB 328 ASSASLEBRKMKVQSITOR--FRLSRDKVAKSIALIIVSIFGLCMAPYLLMITIRACH 385
QY 333 RTERKXSWYSIAFWLQFNFPVNPFLYPLCHRRQKAFMKLCTYK 379
DB 386 GHCVF-DWYETSFVLLMANSVNPVLPCHYSPRRAPYKLLCPQK 431
RESULT 9
ID ID      PRELIMINARY; PRT; 445 AA.
AC AC      Q865E1;
DT DT      01-JUN-2003 (TREMBLrel. 24, Created)
DT DT      01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE DE      Histamine receptor H3.
GN GN      Name=HRH3;
OS OS      Macaca mulatta (Rhesus macaque).
OC OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC OC      Cercopithecinae; Macaca.
OX OX      NCBI_TaxId=9544;
RN RN      (1)
RP RP      SEQUENCE FROM N. A.
RA RA      Yao B.B., Sharma R., Caesar S., Ebenhade T.A., Hancock A.A.;
RL RL      Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
CC CC      -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC CC      -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR DR      EMBL; AY231164; AA063757.1; -.
DR DR      GO; GO:0016021; C:Integral to membrane; IEA.
DR DR      GO; GO:0004969; F:histamine receptor activity; IEA.
DR DR      GO; GO:0004872; F:receptor activity; IEA.
DR DR      GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR DR      GO; GO:0007186; F:G-protein coupled receptor protein signalin...; IEA.
DR DR      InterPro; IPR00276; GPCR_Rhodopsn.
DR DR      InterPro; IPR003980; H3_receptor.
DR DR      Pfam; PF00001; 7tm.1; 1.
DR DR      PRINTS; PR00237; GPCR_RHODOPSIN.
DR DR      PRINTS; PR01471; HISTAMINEH3R.
DR DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR DR      PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW KW      G-protein coupled receptor; Transmembrane.
SQ SQ      SEQUENCE 445 AA; 48591 MW; E79440A4EC09CA8C CRC64;
Query Match 35.1%; Score 718.5; DB 2; Length 445;
Best Local Similarity 38.7%; Pred. No. 2,5e-39;
Matches 163; Conservative 52; Mismatches 121; Indels 85; Gaps 9;
QY 18 LAFLMSFAFIMGNVAVIIAFVVDRLRHSNYFFLNLASDFVLGLISIPLYIPHYL 77
DB 37 LAALMALIIVATVGNALVMLAFVADSLRQNNFFLNLAIISDFVGFICPLVYPVYL 96
QY 78 F-ANNFGSGICMFILITDYLLCTASVYNIIVLISYDRYOSVSNVSYRAOHGIMKIVAQ 136
DB 97 TGRWTFGRGLCKMLVVDYLLCTSSAFNIVLISYDRFVSVTRAAYSRAOQSDTRAAVRKM 156
QY 137 VAVVILAFVNGPMILASDSMK-----NSTWTKDCEPFVTEWYILITITMLLEFLLPYIS 191
DB 157 LLVVVLAFVLYGPAL---SWEYLSGSSIPBGHCYAFEFYNNWYLLTASTLEFPTPLS 213
QY 192 VAVFNVQY-----WSLWKRRALSRCPSH 215
DB 214 VTFPNLSIYLNIOQRTRLRLDGAAREAGPDPPEAQSPPPPPCGCMGCMQGGHGAAMPLH 273
QY 216 -----AGFTTSSASGHLRAGVACRTSNPGLKESASRHSSEPRRKSILVLSIRT 267
DB 274 RYGVGEAAMAGAEETALGGGGGSAASPTSSSG-----SSRGTGERP----- 318

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Oy 268 HNNSSITLFFKVSFMRSESAALROR-----EVAEILRGKCLARSALITLAPALCM 313
Db 319 -----SLKRSKXSASASALEKRMKMSQSSTQFRLSRBRKXAKSLAVISITGLCW 371
Oy 319 APYCLFTIVLSTYPTREPKSVWYSIAFWLQFNSFVNFLYPLCHRRPQKAFKILCVT 378
Db 372 APYTLMLIIRACHGHCHVP-DYWYERSFWLLMANSVNVLYLVLGHHSFRRAPTLLCPQ 430
Oy 379 K 379
Db 431 K 431

RESULT 10
HH3R_RAT
ID HH3R_RAT STANDARD; PRT; 445 AA.
AC OQYVn8; OQYVn6; OQYVn7; OQYVn9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Histamine H3 receptor (HH3R).
GN Name=Hh3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hypothalamus;
RX MEDLINE=20330707; PubMed=10869375;
RA Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;
RT "Cloning of rat histamine H3 receptor reveals distinct species
RL pharmacological profiles.";
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Striatum;
RX MEDLINE=22016732; PubMed=11130725; DOI=10.1038/35048583;
RA Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Jacombe J.,
RA Stark H., Schumack W., Ganelin C.R., Schwartz J.-C., Arrang J.-M.;
RT "High constitutive activity of native H3 receptors regulates histamine
RL neurons in brain.";
RN [3]
RX Nature 408:860-864(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RA Itadani H., Takimura T., Nakamura T., Ohta M.;
RT "Cloning of a novel G protein-coupled receptor";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBD databases.
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=99278519; PubMed=10347254;
RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
RA Huyar A., Jackson M.R., Erlander M.G.;
RT "Cloning and functional expression of the human histamine H3
RL receptor.";
RN [5]
RX Mol. Pharmacol. 55:1101-1107(1999).
RN [5]
RP FUNCTION: The H3 subclasses of histamine receptors could mediate the
RL histamine signals in CNS and peripheral nervous system. Signals
RL through the inhibition of adenylyl cyclase and displays high
RL constitutive activity (spontaneous activity in the absence of
RL agonist).
RN [5]
RP SUBCELLULAR LOCATION: Integral membrane protein.
RN [5]
RP ALTERNATIVE PRODUCTS:
RL Event=Alternative splicing; Named isoforms=4;
RL Comment=Additional isoforms seem to exist;
RN [5]
RP Name=1; Synonyms=H3L;
RL Name=2; Synonyms=H3S;
RN [5]
RP Name=3;
RL Name=4;
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	-1- TISSUE SPECIFICITY:	Expressed abundantly in brain, most notably throughout the thalamus, the ventromedial hypothalamus and the caudate nucleus. Isoform 1 is largely predominant in all tissues.
	-1- MISCELLANEOUS:	Poxyfinan acts as a potent neutral antagonist while ciloperamide, ciproxifan and FUR645 act as potent inverse agonists.
	-1- SIMILARITY:	Belongs to the G-protein coupled receptor 1 family.
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	EMBL	, AF279191; AAF82086.1; -
	DR	EMBL; AY009370; AAAK02069.1; -
	DR	EMBL; AB015646; BAA88765.1; -
	DR	EMBL; AB015646; BAA88766.1; -
	DR	EMBL; AB015646; BAA88767.1; -
	DR	EMBL; AB015646; BAA88768.1; -
	DR	RSD; 620630; Hrn3.
	DR	InterPro; IPR000276; GPCR_Rhodopsin.
	DR	InterPro; IPR003980; H3_receptor.
	DR	Pfam; PF00001; 7tm_1; 1.
	DR	PRINTS; PR00237; GPCCRHOOPSN.
	DR	PRINTS; PR01471; HISTAMINEH3R.
	DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
	DR	PROSITE; PS02062; G_PROTEIN_RECEP_F1_2; 1.
	KW	. Alternative splicing; G-protein coupled receptor; Glycoprotein; Transmembrane.
FT	DOMAIN	1 39 Extracellular (Potential).
FT	TRANSMEM	40 60 Potential.
FT	DOMAIN	61 70 Cytoplasmic (Potential).
FT	TRANSMEM	71 91 Potential.
FT	DOMAIN	92 108 Extracellular (Potential).
FT	TRANSMEM	109 129 Potential.
FT	DOMAIN	130 156 Cytoplasmic (Potential).
FT	TRANSMEM	157 177 Potential.
FT	DOMAIN	178 196 Extracellular (Potential).
FT	TRANSMEM	197 217 Potential.
FT	DOMAIN	218 359 Cytoplasmic (Potential).
FT	TRANSMEM	360 380 Potential.
FT	DOMAIN	381 396 Extracellular (Potential).
FT	TRANSMEM	397 417 Potential.
FT	DOMAIN	418 445 Cytoplasmic (Potential).
FT	CARBOHYD	20 23 Poly-Ala.
FT	TRANSPLIC	11 11 N-linked (GlcNAc . .) (Potential). Missing (in isoform 2).
FT	VARSPLIC	274 305 Missing (in isoform 3 and isoform 4).
FT	TRANSPOLC	274 321 Missing (in isoform 3 and isoform 4).
FT	VARSPLIC	393 445 WTSPFWLTWNASVNPVLPLYCHYSRRRTATKLCPQPK VDPHSLEQCWK -> CVERIGKEASLLPLPMFSGWR RAEHVCELDIPWMFNQRONCRGARGWIGRCGLPPPSVQL LPAEVPRLLPAPPGLGRMPCACPVTIRIMGVVMVG (in isoform 4).
FT	SEQUENCE	445 AA; 4858 MW; 63DFEEFC2I758FESEB CRC64; /ftid=vsp_001889.
OY	Query Match	35.0%; Score 716.5; DB 1; Length 445;
Dd	Beat Local Similarity	40.2%; Pred. No. 3.3e-39;
Matches	165; Conservative	54; Mismatches 128; Indels 63; Gaps 10;
Oy	18 LAPMSFAPIFMGAIVIAFLVDNRLRKSRYFFLNLAISPLYLGIPIFYIPVL	77
Dd	37 LAALMALLIYAIVTGNALVMAFDADSLRKQNPFLLNLAIISPFLYGACIPYIPVYL	96
Oy	78 F-NNNFGSIGMFLLTDYYLLCTAAYNYIVLSIDRVOSVSNAVSYPAROHGMKIQAQM	136
Dd	97 TGERTTFGGRLCKMLNDVDTLCASSVENVIULSIDRFSTSVRAVSYAPAQGDTRAAVAKM	156

QY 137 VAVWTLAFLVNGPMILASDSWK-----NSTNTKDCPEGFVTEWYLTITMLLEFLPVIS 191  
 DB 157 ALVWTLAFLVNGPALI-----SWEYLSGSGSIPBGHCIAEFYVNWYFLITASTLEFPTPLS 213  
 QY 192 VAVFVVOIYWSLMKRAL-----SRCPSHAGFSTSSASAGH-----LH 230  
 DB 214 VTFPFLSLIYLNIOQRTRRLDGRAGREAGPEPPDAQPPAPPPSCWGCMPKGGHGAEMPLH 273  
 QY 231 RAGVACRTSNPGLK-----ESASRHSBSPRRKSSILVSLRTM 269  
 DB 274 RYGVG-EGCPGEVEGEALAGSGGGGAASPTSSSGSSRGTERRP-----SLKRGSK 324  
 QY 270 NSSITAFKVSFWRSESAALROREYAEILGRKRLASLAILLSAFALCWAPYCLFTYVLS 329  
 DB 325 KPSASASLEKRMKWSQISITQR--FRLSRDKKVAKSALIIYSIGLCAPYTLMLITRA 382  
 QY 330 TYPRTERPKSVWSIAFWLQWNSFVNPFYPLCHRRFOKAFKILCVTK 379  
 DB 383 ACHGRGCP-DWYETSFMLMANSVNPVLYPLCHYSFRRAFTKLCPQK 431

RESULT 11

HH3R MOUSE STANDARD; PRT; 445 AA.  
 AC P58406;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Histamine H3 receptor (HH3R).  
 GN Name=Hh3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CD-1;  
 RA Coge F., Rigue H., Levecher B., Leopold O., Guenin S.-P., Boutin J.A.,  
 RA Galizzi J.-P.,  
 RT "Cloning of mouse histamine H3 receptor."  
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: The H3 subclass of histamine receptors could mediate the  
 CC histamine signals in CNS and peripheral nervous system. Signals  
 CC through the inhibition of adenylylase activity and displays high  
 CC constitutive activity (spontaneous activity in the absence of  
 CC agonist) (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; AY044153; AAK72406.1; -.  
 DR MGD; MGI:2139279; Hh3;  
 DR InterPro; IPR000376; GPCR Rhodopsin.  
 DR InterPro; IPR003980; H3\_receptor.  
 DR Pfam; PF00001; 7tm\_1; 1  
 DR PRINTS; PR00237; GPCRHHODOPSIN.  
 DR PRINTS; PR01471; HISTAMINER3.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
 FT DOMAIN 1 39 Extracellular (Potential).  
 FT TRANSMEM 40 60 Potential.  
 FT DOMAIN 61 70 Cytoplasmic (Potential).  
 FT TRANSMEM 71 91 Potential.  
 FT DOMAIN 92 108 Extracellular (Potential).  
 FT TRANSMEM 109 129 Potential.

FT DOMAIN 130 156 Cytoplasmic (Potential).  
 FT TRANSMEM 157 177 Potential.  
 FT DOMAIN 178 196 Extracellular (Potential).  
 FT TRANSMEM 197 217 Potential.  
 FT DOMAIN 218 239 Cytoplasmic (Potential).  
 FT TRANSMEM 240 260 Potential.  
 FT DOMAIN 261 281 Extracellular (Potential).  
 FT TRANSMEM 282 302 Potential.  
 FT DOMAIN 303 323 Cytoplasmic (Potential).  
 FT TRANSMEM 324 344 Potential.  
 FT DOMAIN 345 365 Poly-Ala.  
 FT CARBOHD 366 386 N-linked (GlcNAc...)(Potential).  
 FT SEQUENCE 387 445 AA; 48541 MW; 88D406E29E1F3C5F CRC64;

Query Match 34.9%; Score 715.5; DB 1; Length 445;  
 Beet Local Similarity 40.7%; Pred. No. 3.9e-39;  
 Matches 166; Conservative 51; Mismatches 132; Indels 59; Gaps 10;

QY 18 LAFWMSFAFIMVGNVAVIILAFVVDRLRRHSNYFFPLNALISDFVLISIPLYPVYL 77  
 DB 37 LAALMALIIVATVVLGNALVMLAFVADSSLRTQNNPFLNLALISDFVLGAFICILVVPVYL 96  
 QY 78 F-MNFGSGICMFWLITDYLLCTASVNIILSYDROSVSNASVRAQHTGIMKIVAQ 136  
 DB 97 TGRMTFFGRGLCKMLVVDYLLCASSVFNIILSYDRLVTRAVSYRAQGDTRRAVRKM 156  
 QY 137 VAVWTLAFLVNGPMILASDSWK-----NSTNTKDCPEGFVTEWYLTITMLLEFLPVIS 191  
 DB 157 ALVWTLAFLVNGPALI-----SWEYLSGSGSIPBGHCIAEFYVNWYFLITASTLEFPTPLS 213  
 QY 192 VAVFVVOIYWSLMKRAL-----SRCPSHAGFSTSSASAGH-----LH 230  
 DB 214 VTFPFLSLIYLNIOQRTRRLDGRAGREAGPEPPDAQPPAPPPSCWGCMPKGGHGAEMPLH 273  
 QY 231 R-----AGVACRTSNPGL-----KESASRHSBSPRRKSSILVSLRTMNS 271  
 DB 274 RYGVG-EGCPGEVEGEALAGSGGGGAASPTSSSGSSRGTERRP-----SLKRGSKP 326  
 QY 270 NSSITAFKVSFWRSESAALROREYAEILGRKRLASLAILLSAFALCWAPYCLFTYVLS 329  
 DB 325 KPSASASLEKRMKWSQISITQR--FRLSRDKKVAKSALIIYSIGLCAPYTLMLITRA 384  
 QY 330 TYPRTERPKSVWSIAFWLQWNSFVNPFYPLCHRRFOKAFKILCVTK 379  
 DB 383 ACHGRGCP-DWYETSFMLMANSVNPVLYPLCHYSFRRAFTKLCPQK 431

RESULT 12

06ZM33 PRELIMINARY; PRT; 473 AA.  
 AC 06ZM33;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE S1:bz3AG2.4 (Novel protein similar to human histamine receptor H3  
 DE (HH3)).  
 GN Name=S1:rp71-34g2.4; Synonyms=S1:bz3AG2.4;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NC NCB1\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tracey A.;  
 RL Submitted (OCT-2003) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC EMBL; AL928906; CAB9228.1; -.  
 DR ZFIN; ZDB-GENE-040724-204; S1:rp71-34g2.4.  
 DR GO; GO:0016021; C:Integral to membrane; IEA.  
 DR GO; GO:0004969; F:histamine receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.









GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 6, 2005, 19:33:07 ; Search time 5685 Seconds  
(without alignments)  
3332.628 Million cell updates/sec

Title: US-10-626-445-8  
Perfect score: 2048  
Sequence: 1 MSENSTGILPPAAQVPLA.....WKLCVTKMPALSNQSVSS 391

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-DB=GenEmbl -QFMT=fastap -SUFFIX=rg -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human0.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=Pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:.\*  
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2: gb\_hcg:.\*  
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13: gb\_un:.\*  
14: gb\_vl:.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2035	99.4	1538	10	AF358859 Mus muscu
2	1745	85.2	1593	10	AF358860 Rattus no
3	1434.5	70.0	199837	10	AC131672 Mus muscu
4	1372.5	67.0	1173	9	AY008280 Homo sapi

5	1370.5	66.9	1173	6	AR142850	Sequence
6	1370.5	66.9	1173	6	AR391860	Sequence
7	1370.5	66.9	1173	6	AX109119	Sequence
8	1370.5	66.9	1173	6	AX139113	Sequence
9	1370.5	66.9	1173	6	AX301763	Sequence
10	1370.5	66.9	1173	6	BD015847	Novel pol
11	1370.5	66.9	1173	9	AF307973	Homo sapi
12	1370.5	66.9	1173	9	AF325356	Homo sapi
13	1370.5	66.9	1173	9	AF329449	Homo sapi
14	1370.5	66.9	1173	9	AY136745	Homo sapi
15	1370.5	66.9	1173	9	HS4298292	Homo sapi
16	1370.5	66.9	1266	6	AX376577	Sequence
17	1370.5	66.9	1300	6	AX301229	Sequence
18	1370.5	66.9	1312	6	BD095598	Novel gna
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21	1370.5	66.9	3689	6	AX549343	Sequence
22	1370.5	66.9	3689	9	AF312230	Homo sapi
23	1366.5	66.7	1227	6	BD097512	Novel gna
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25	1311.5	64.0	1291	4	AB053300	Sub gctof
26	1238	60.4	1451	10	AF358858	Sequence
27	1199	58.5	236694	2	AC118386	Cavla por
28	906	44.2	140555	9	AC007922	Rattus no
29	906	44.2	166206	2	AC009668	Homo sapi
30	906	44.2	167296	2	AP002507	Homo sapi
31	906	44.2	169144	2	AC090244	Homo sapi
32	906	44.2	184938	2	AP002476	Homo sapi
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## ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION Mus musculus histamine H4 receptor mRNA, complete cds.  
ACCESSION AF358859  
VERSION AF358859.1 GI:15420534  
KEYWORDS  
SOURCE  
ORGANISM Mus musculus (house mouse)

REFERENCE  
AUTHORS Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.  
TITLE 1 (bases 1 to 1538)  
JOURNAL 2 (bases 1 to 1538)  
REFERENCE  
AUTHORS Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.  
TITLE Direct Submission  
JOURNAL Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson  
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,  
CA 92121, USA

FEATURES  
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CDS

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/db\_xref="GI:15420535"  
/translation="MSESNSTGILPPAAQVPLAFIMSSFAFMGNVILAFVADR  
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TNTKDEPGFVTEWYIILITMLLEFLIPVAVENVOIYSLMKRSLRCSHGAF  
STSSASAGHLRAGVACRTSNRPGKESASRHSRPSRLSTLNTMNSSTAF  
KVSFMRSESAALRQREYAEILRGRKLARSALILLSAFALCMAPYCLFTIVSTYRPT  
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ORIGIN

Alignment Scores:

Score:	3.42e-155	Length:	1538
Percent Similarity:	2035.00	Matches:	390
Best Local Similarity:	99.74%	Conservative:	0
Query Match:	99.74%	Mismatches:	1
	99.37%	Indels:	0
	10	Gaps:	0

US-10-626-445-8 (1-391) x AF358859 (1-1538)

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Db 61 ATGTGGAGCTAAAGTACTGGCATCTTCCACACACTGCTCAAGTCCCTGGCATTT 120  
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyValAlaValIleLeuAlaPhe 40  
Db 121 TTAATGCTTCATTTGGCTTGGCTATATAGTAGGCATATCTGCTGATCTTACCTTT 180  
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnThrPhePheLeuAlaLeuAlaSer 60  
Db 181 GTGTGGACGAACCTTAACATCGAAGATATATTTTCTTAATTTGGCTATTTCT 240  
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrlleProHisValLeuPheAsnTrp 80  
Db 241 GACTTCCTGGTGGTTGATTTCATTCCTCTGACATCCCTCAACGTTGTTAACTGG 300  
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrlleLeuLeuGlyThrAla 100  
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Qy 101 SerValTyrlleValIleLeuIleSerTyrlleAspArgTyrlleGlnSerValSerAlaVal 120  
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Qy 121 SerTyrlleArgAlaGlnHisThrGlyIleMetLeuValIleValAlaGlnMetValAlaValTrp 140  
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Db 481 ATATCGGCTTTCTGTGTAATGGCCCGATATCTGGCTTCAGATTTCTTGAAGAAGCAGC 540  
Qy 161 ThrAsnThrTyrlleAspCysGlnProGlyPheValThrGlnTyrlleLeuThrIleThr 180  
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Db 661 TGGAGCTGTGGAAGCTAGGCTCTCAGTAGGAGCCCTAGCCATGTGTGATTTCTCACT 720  
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaValAlaCysValGlnTrpSerAsn 240  
Db 721 ACCTTTCCAGTCTTCAGACACTTAACACAGAGCTGGGGTGGCTTGCAGACCAAGTAAT 780

Qy 241 ProGlyLeuIleuGluSerAlaAlaSerArgHisSerGluSerProAlaArgIleuSerSer 260  
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Qy 261 IleLeuValSerLeuArgThrHisMetLeuSerSerIleThrAlaPheValGlySer 280  
Db 841 ATCTGTGTCTCTTAAGAGACTCAAGAACAGAGATATCACTGCTTCAAAAGTGGGTTC 900  
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGlnTyrlleValIleLeuLeuArgGly 300  
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Qy 301 ArgIleLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
Db 961 AGGAAGCTAGCCAGGCTCATCGGCCATCTTCTAGCGCTTTCATTTGCTGGCTCCA 1020  
Qy 321 TyrlleValLeuPheThrIleValLeuSerThrTyrlleProArgThrGlnArgProIleSerVal 340  
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Qy 341 TrpTyrlleSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrlle 360  
Db 1081 TGGTACAGCATTCCTCTTGGCTGCAATGCTTCAATTCCTTTGTTAATCCCTTCTGTAC 1140  
Qy 361 ProLeuGlyHisArgArgPheGlnIleValaPheTrpIleLeuGlyValIleTyrlleTrp 380  
Db 1141 CTTTGTGTGACACAGGCGTTTCCAGAAAGCTTCTTGAAGATATCTTGTGACAAAGCAA 1200  
Qy 381 ProAlaLeuSerGlnHisGlnSerValSerSer 391  
Db 1201 CCAGCGCTGTCAACAGAACAGATCATATCTTCT 1233

RESULT 2

AF358860 1593 bp mRNA linear ROD 02-SEP-2001  
LOCUS AF358860  
DEFINITION Rattus norvegicus histamine H4 receptor mRNA, complete cds.  
ACCESSION AF358860.1 GI:15420536  
VERSION  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 1593)  
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1593)  
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Direct Submission  
JOURNAL Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA

FEATURES

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## ORIGIN

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## Alignment Scores:

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Score:	89.264	Conservative:	17
Best Local Similarity:	84.914	Mismatches:	42
Query Match:	85.214	Indels:	0
DB:	10	Gaps:	0

US-10-626-445-8 (1-391) x AF358860 (1-1593)

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DB 96 TTAATGTCCCTGCTTGTCTTGTATAGAGATAGGCAATGCTGTGCTATTTAGCCTTT 155
QY 41 ValIleAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB 156 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTATTTTCTTAATTGGCTATTCT 215
QY 61 AppPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIlePheAsnTyr 80
DB 216 GACTCTTCTGTGGTGTCTATCTCCATCTCTGTATACCTCCACAGCTGTTTAACTGG 275
QY 81 AsnPheGlySerGlyIleCysMetPheTyrPheIleThrAspTyrLeuLeuGlyThrAla 100
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QY 101 SerValTyrAsnIleValIleuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
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QY 121 SerTyrArgAlaGlnHisThrGlyIleMetValIleValIleGlnMetValAlaValTyr 140
DB 396 CCTTATAGACACAGACACTGACATCGCAATATGTTGCTCAAAATGGTGGCTGTGTTGG 455
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrAsnSer 160
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QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTyrIleLeuThrIleThr 180
DB 516 ACCAACAACAGAGAGAGCGAGCGCTGCTTGTATAGAGTGTATACATCTCCCATTTACA 575
QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
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QY 201 TTPSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
DB 636 TGGACCTCTGGAAGGTGGAGTCTCATAGTGTGCTTACGACACGCTGGATTCATCGT 695
QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
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QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
DB 816 CTCCTGCTGTCTCTTAAGACATCATAGACGCTAGATATATGCTTCAAAAGTGGTTC 875
QY 281 PheTyrArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
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QY 321 TyrCysLeuPheThrIleValIleuSerThrTyrProArgThrGluArgProLysSerVal 340
DB 996 TATTCCTGCTTACATATGTTCTTCACTTATTCACAGAGGAGGAGCGCCCAATCGATT 1055
QY 341 TrrPyrSerIleAlaPheThrLeuLntPheAsnSerPheValAsnProPheLeuTyr 360
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QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTyrPlyIleLeuCysValThrLysTyr 380
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## RESULT 3

AC131672/c

AC131672 199837 bp DNA linear ROD 11-FEB-2004

AC131672 Mus musculus chromosome UNK clone RP23-314021, complete sequence.

AC131672.3 GI:42517281

HTG. Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 199837)

Wilson, R.K.

The sequence of Mus musculus clone

Unpublished

2 (bases 1 to 199837)

McPherson, J.D. and Waterson, R.H.

Direct Submission

Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

3 (bases 1 to 199837)

Wilson, R.K.

Direct Submission

Submitted (11-FEB-2004) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

On Feb 11, 2004 this sequence version replaced gi:38194370.

COMMENT

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu

Contact: submissions@wustl.edu

Project Information -----

Center project name: M BA0314021

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Location/Qualifiers

1. 199837

/organism="Mus musculus"

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/chromosome="UNK"

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ORIGIN

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Pred. No.:

Score:

Percent Similarity:

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78.634

Length:

Matches:

Conservative:

199837

296

13

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Query Match: 70.04%  Indels: 51
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US-10-626-445-8 (1-391) x AC131672 (1-199837)

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Qy 24 SerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIleLeuAlaPheValAlaAsp 43
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Qy 99 ThrAlaSerValTyRasIleValIleSerTyRasPargTyRginSerValSerAsn 118
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Qy 159 AsnSerThrAsnTrpLysAspCysGluProGlyPheValThrGluTrpTyRileLeuThr 178
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Qy 179 IleThrMetLeuLeuGluPheLeuLeuProValIleSerValAlaTyRAsnValGln 198
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RESULT 4
LOCUS AY008280 1173 bp mRNA linear PRI 15-MAR-2004
DEFINITION Homo sapiens histamine receptor H4 (H4) mRNA, complete cds.
ACCESSION AY008280
VERSION AY008280.1 GI:15822540
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Nguyen,T., Shapiro,D.A., George,S.R., Setola,V., Lee,D.K.,
Cheng,R., Rauser,L., Lee,S.P., Lynch,K.R., Roth,B.L. and
O'Dowd,B.F.
Discovery of a novel member of the histamine receptor family
Mol. Pharmacol. 59 (3), 427-433 (2001)
JOURNAL MEDLINE 21106319
PUBMED 11179435
AUTHORS Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and
O'Dowd,B.F.
Discovery of H4, a Novel Histamine Receptor
Unpublished
3 (bases 1 to 1173)
REFERENCE Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and
O'Dowd,B.F.
Direct Submission
Submitted (26-SEP-2000) Pharmacology, University of Toronto, 8
Taddle Creek Rd., Rm. 4353, Toronto, Ont M5S 1A8, Canada
JOURNAL Location/Qualifiers
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Query Match: 67.02% Indels: 3

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DB	61	TTTATGTCCTTAGTACTTTTGCTATTAAGCTAGAAATGCTTGG	TATAGCTTTT 120
OY	41	ValIValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeu	MetLeuAlaIleSer 60
DB	121	GGGGGAGCAAAAACCTTAGACATCGAAGATTAATTTTCTTAAC	TTGGCCATCTCT 180
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DB	181	GACCTCTTGTGGGTGTGATCTCCATCTCTTTGATCAATCCCTCA	CACAGCTGTTCGAAATGG 240
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OY	121	SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGln	MetValAlaValATP 140
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OY	201	TyrSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAla	GlyPheSerThr 220
DB	595	TGGACCTGTGGAGAGGTGATCATCTCACTAGGTGCAAGCATCT	GTGACATGATGCT 654
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DB	715	TCTGCATGCACGAAGTTCCTGATCTCTTCAATTCAGAGACAGAG	AGGAAAGATAGT 774
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VERSION	AR142850.1	GI:15104136	
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REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1173)		
	Behan, J.K., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L.,		
TITLE	Unland, S.P. and Wang, S.		
JOURNAL	Polynucleotide encoding a histamine receptor		
FEATURES	Patent: US 6204017-A 1 20-MAR-2001;		
	Location/Qualifiers		
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Best Local Similarity:	68.11%	Mismatches:	82
Query Match:	66.92%	Indels:	3
Db:	6	Gaps:	2
US-10-626-445-8 (1-391) x AR142850 (1-1173)			
Qy	1	MeScerGluSerAaSerThrGlyIleLeuProProAlaAaGlnValProLeuAlaPhe	20
Db	1	ATGCGCAATATCTAATAGCACAAATCAATTTTATCACTAAGCACTGGTTACTTTAGCATTT	60
Qy	21	LeuMetSerSerPheAlaPheAlaIleMetValGlyAaAspIleValIleLeuAlaPhe	40
Db	61	TTTATGTCTTCTAGTACTGTTTGTCTATATATCTTGAAGAAATCTTGGTCAATTTAGCTTTT	120
Qy	41	ValValAspArgAaLeuAaRgHiSaRgSerAaSerTrpPhePheLeuAaLeuAlaIleSer	60
Db	121	GTGGTGCACAAAACCTTACATCAGACAGTAAAGTATATTTTCTTAACTTGGCATCTCT	180
Qy	61	AaPheLeuValGlyIleuIleSerIleProLeuTrpIleProHiSValLeuPheAaTrp	80
Db	181	GACTTCTTTGTGGGTGATCTCCATCTCCTTTGTACATCCCTCACACGCTTGCAATGG	240
Qy	81	AaAspPheGlySerGlyIleCyMetCysPheTrpLeuIleThrAspTrpLeuLeuCyThrAla	100
Db	241	GATTTTGGAAAAGAAATCTGTATTTTGGCTCACTACGACATATCTGTATATGACGCA	300
Qy	101	SerValTrpAaIleValIleuIleSerTrpAspArgTrpGlnSerValSerAaAlaVal	120
Db	301	TCTGTATTAATCAATGTGCTTCATCAGCTAAGATCGATCTGTCAGTCTCAAAATGCTGTG	360
Qy	121	SerTrpArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp	140
Db	361	TCTTATGAACTCAACATCTGGGGCTTGAAGATGTACTCTGATGATGGCGGTTTGG	420
Qy	141	IleLeuAlaPheLeuValAaGlyProMetIleLeuAlaSerAspSerTrpIysAaSer	160
Db	421	GTGTGGCCCTTCTTAAGATGGGCAATGATTCGTGTTGACAGTCTTGGAAAGATGAA	480

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      535 TCATTTCTGGAAATTCGATGCCGATCTTACTGCTTATTTCAACATGAAATATTAT 594
Qy      201 TrpSerLeuTrpIysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
      595 TGGAGCTGTGGAAAGCGGATCATCTAGTAGGCGCAAGCCATCTGGACGTGACGTCT 654
Qy      221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
      655 GTCTCTTCCAACATCTGGACATCTCACTCAAGAGTAGACTATCTCAAGAGATCTCTT 714
Qy      241 ProGlyLeuLeuGluSerAlaAlaSerArgHisSerGluSerProArgArgGlySerSer 260
      715 TCTGCATCGACAGAAAGTTCCCTGCTCTTCATTCACAGACAGACAGAGAGAGTAGT 774
Qy      261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
      775 CTATGTTTTCCTCAAGAACAGATGAATGACATGCAATGCTCTCCAAATGGGTCC 834
Qy      281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
      835 TTCTCCCAATCAGATTTCTGATAGCTCTTCACCAAGGGAACATGTGAACTGCTTAGGCC 894
Qy      301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
      895 AGAAGATTAGCCAAAGTCACTGGCCATTCCTTAGGGGTTTTTGCTGTGCTGGGCTCCA 954
Qy      321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
      955 TATCTCTGTCACAATTCCTTCATTTATTTCTCCAGAACAGGTCTCTAAATTCAGTT 1014
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Qy      361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
      1075 CCAATTGTGTCAACGCCCTTCAAAAGCTTTCTTGAATAATTTGTATATAAAAGCAA 1134
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RESULT 6
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LOCUS      AR391860
DEFINITION      Sequence 1 from patent US 6613533.
ACCESSION      AR391860
VERSION      AR391860.1  GI:40115568
KEYWORDS
SOURCE
ORGANISM      Unknown.
                Unclassified.
REFERENCE
AUTHORS      1 (bases 1 to 1173)
                Behan, J. X., Hedrick, J. A., Laz, T. M., Monsma, F. J., Morse, K. L.,
                Umland, S. P. and Wang, S.
TITLE      Histamine receptor
JOURNAL      Patent: US 6613533-A 1 02-SEP-2003;
FEATURES
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ORIGIN
Alignment Scores:      1,586-101      Length:      1173
Pred. No.:      1370.50      Matches:      267
Score:

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Percent Similarity:      78.32%      Conservative:      40
Best Local Similarity:      68.11%      Mismatches:      82
Query Match:      66.92%      Indels:      3
DB:      6      Gaps:      2

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US-10-626-445-8 (1-391) x AR391860 (1-1173)

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      61 TTATATGCTCTTACTAGCTTTTGCTATTAATGCTGAAATGCTTTGGTCACTTTAGCTTTT 120
Qy      41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
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      181 GACTTCTTTGTGGTGTGATCTTCATCTCTTTGTACATCCCTCAACGCGTTTCGAATGG 240
Qy      81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleLeuLeuCysThrAla 100
      241 GATTTGGAAAGAAATCTGTGATTTTGGCTCACTAGTCACTATCTGTTATGTACAGCA 300
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      481 GGTAGT-----GAAATGAACTGGAAATTTTTCGAAATGGTACATCTCTGCCATCA 534
Qy      181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
      535 TCATTTCTGGAAATTCGATTCGCCAGTCACTTATAGTGGCTTATTTCAACATGAAATATTAT 594
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 ACCESSION  
 VERSION AX109119.1 GI:13924093  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE 1 Behn, J. X., Hedrick, J. A., Laz, T. M., Monema, F. J., Morse, K. L.,  
 Umland, S. and Wang, S.  
 TITLE Histamine receptor  
 JOURNAL Patent: WO 0125432-A 1 12-APR-2001;  
 SHERING CORPORATION (US)  
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 Alignment Scores:  
 Pred. No.: 1.58e-101 Length: 1173  
 Score: 1370.50 Matches: 267  
 Percent Similarity: 78.32% Conservative: 40  
 Best Local Similarity: 68.11% Mismatches: 82  
 Query Match: 66.92% Indels: 3  
 DB: Gaps: 2  
 US-10-626-445-8 (1-391) x AX109119 (1-1173)  
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 Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAaAlaValAlaIleLeuAlaPhe 40  
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 Qy 41 ValValAaPArgAaLeuLeuArgH1aAArgPheGlnValAlaPheTrpValIleLeuCyValThrIleTrp 60  
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 Db 421 GTGCTGCGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 Qy 161 ThrAaThrIleAaPArgGlyProGlyIleValIleTrpIleTrpIleLeuThrIleThr 180  
 Db 481 GGTAGT-----GAATGTAACTGATTTTGTGAAATGATGATGATGATGATGATGATGATGATGATGAT 534  
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 Db 535 TCATCTTGAT 594  
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 ACCESSION  
 VERSION AX139113.1 GI:14274791  
 KEYWORDS  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 Peter, B. and O'Reilly, M. A.  
 TITLE G-protein coupled receptor-like polypeptide  
 JOURNAL Patent: EP 1096009-A 1 02-MAY-2001;  
 Pfizer Limited (GB) ; PFIZER INC. (US)  
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## Alignment Scores:

Pred. No.: 1,586-101 Length: 1173  
Score: 1370.50 Matches: 267  
Percent Similarity: 78.32% Conservative: 40  
Best Local Similarity: 68.11% Mismatches: 82  
Query Match: 66.92% Indels: 3  
DB: 6 Gaps: 2

US-10-626-445-8 (1-391) x AX139113 (1-1173)

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Db 421 GTGCTGCTCTTCTTAGAGTAATGGCCAAATGATTTCTACAGCTTTGGAAGATGAA 480  
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RESULT 9  
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LOCUS  
DEFINITION  
Sequence 1 from Patent WO185786.  
AX301763  
VERSION  
AX301763.1 GI:17382844  
KEYWORDS  
SOURCE  
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ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
1 Jones, P. G., Blatcher, M., Wu, S. and Pausch, M. H.  
Human histamine h 4f receptor  
Patent: WO 0185786-A 1 15-NOV-2001,  
JOURNAL  
American Home Products Corporation (US)  
Location/Qualifiers  
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ORIGIN

Alignment Scores:

Pred. No.: 1,586-101 Length: 1173  
Score: 1370.50 Matches: 267  
Percent Similarity: 78.32% Conservative: 40  
Best Local Similarity: 68.11% Mismatches: 82  
Query Match: 66.92% Indels: 3  
DB: 6 Gaps: 2

US-10-626-445-8 (1-391) x AX301763 (1-1173)

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Db      481 GGTAGT-----GAATGTAACCTGATATTTTTCGAATGGTACATCTTCCATCACA 534
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DEFINITION Novel polypeptide.
ACCESSION  BD015847
VERSION    BD015847.1 GI:22556984
KEYWORDS   JP 2001211889-A/1.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
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REFERENCE  1 (bases 1 to 1173)
AUTHORS   Peter B. and Olajide, M.A.
TITLE      Novel polypeptide
JOURNAL    Patent: JP 2001211889-A 1 07-AUG-2001;
            PFIZER INC
COMMENT    OS Homo sapiens (human)
            PN JP 2001211889-A/1
            PD 07-AUG-2001
            PE 27-OCT-2000 JP 2000329359
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Score:          1370.50      Matches:      267
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Best Local Similarity: 68.11%      Mismatches: 82
Query Match:    66.92%      Indels:      3
DB:              Gaps:      2

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RESULT 11
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DEFINITION AF307973
ACCESSION AF307973.1 GI:1141732
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Jones, P. G., Wu, S. and Betty, M.
TITLE Cloning of a novel histamine receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1173)
AUTHORS Jones, P. G., Wu, S. and Betty, M.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-2000) Neuroscience, Wyeth Ayerst, CN8000,
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 REFERENCE 1 (bases 1 to 1173)  
 AUTHORS Zhu, Y., Michalovich, D., Wu, H.-D., Tan, K. B., Dyke, G. M., Mannan, I. D., Boyce, R., Alston, J., Tierney, L. A., Li, X., Herlihy, N. C., Wawter, L., Sarau, H. M., Ames, R. S., Davenport, C. M., Hieble, P., Wilson, S., Bergema, D. J. and Fitzgerald, L. R.  
 TITLE Cloning, expression, and pharmacological characterization of a novel human histamine receptor  
 JOURNAL Mol. Pharmacol. 59 (3), 434-441 (2001)  
 MEDLINE 21106320  
 PUBMED 11179436  
 REFERENCE 2 (bases 1 to 1173)  
 AUTHORS Zhu, Y., Michalovich, D. and Fitzgerald, L. R.  
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ACCESSION AF329449.1 GI:13876643
VERSION
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Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A.,
Antbeson, J.C., Umland, S., Wan, Y., Hipkin, R.W., Gonsiorek, W., Shin, N.,
Gustafson, E.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M.,
and Monema, F.J. Jr.
Cloning and characterization of a novel human histamine receptor
J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)
JOURNAL 21104636
MEDLINE 11181941
PUBMED 2 (bases 1 to 1173)
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AUTHORS Bayne, M.
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ORIGIN
Alignment Scores:
Score: 1,586-101 Length: 1173
Pred. No.: 1370.50 Matches: 267
Percent Similarity: 78.32% Conservative: 40
Best Local Similarity: 68.11% Mismatches: 82
Query Match: 66.92% Indels: 3
DB: Gaps: 2
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DB 421 GTCTGGCCCTTCTTGAATGGAATGGCCCAATGATCTAGTTTCAAGCTTGGAAAGTAA 480
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REFERENCE  
 AUTHORS Publ.H.L. III, Ikeda,S.R. and Aronstein,R.S.  
 TITLE Direct Submission  
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REFERENCE
AUTHORS O'Reilly,M.A.
TITLE   Identification of a histamine H4 receptor on human eosinophils -
        Role in eosinophil chemotaxis
JOURNAL Unpublished
AUTHORS O'Reilly,M.A.
TITLE   Direct Submision
JOURNAL Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

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(without alignments)  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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8	1370.5	66.9	1173	5	AA424007
9	1370.5	66.9	1173	6	AB280663
10	1370.5	66.9	1173	6	ABQ78739
11	1370.5	66.9	1173	6	AA170980
12	1370.5	66.9	1173	6	AA167750
13	1370.5	66.9	1173	8	ACA93262
14	1370.5	66.9	1173	10	ADG98759
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## ALIGNMENTS

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AC	AA170981;	
DT	18-MAR-2002	(first entry)
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KW	Histamine H4 receptor; mouse; antihistaminic; antiallergenic; antinflammatory; cardiant; circulatory; antidiabetic; laxative;	
KW	diagnosis; gene therapy; ss.	
OS	Mus musculus.	
XX	WO200192485-A1.	
XX	06-DEC-2001.	
XX	22-FEB-2001; 2001WO-US005914.	
XX	31-MAY-2000; 2000US-0208260P.	
XX	(ORTH ) ORTHO-MCNEIL PHARM INC.	
XX	Lovenberg T, Liu C;	
XX	WPI, 2002-114339/15.	

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AB242533	Human his
ACC59394	Human his
ADD22860	Human ful
ADQ89179	Human uro

DR P-PSDB; AAM50565.

XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
PT the proteins, useful in gene therapy for treating diseases where it is  
PT beneficial to elevate mammalian histamine H4 receptor activity.

PS Claim 4; Fig 5A; 92pp; English.

XX The present sequence is that of a cDNA clone encoding a murine histamine  
CC receptor of the H4 subtype. The cDNA was isolated from a murine spleen  
CC cDNA library. It shows 72.8% homology to the human H4 receptor coding  
CC region. The invention provides mammalian (human, mouse, rat and guinea  
CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
CC recombinant host cells that produce active recombinant protein. The  
CC pharmacology of known histamine ligands is demonstrated. Mammalian  
CC histamine H4 receptor may be used in gene therapy for the treatment of  
CC diseases where it is beneficial to elevate mammalian histamine H4  
CC receptor activity. Recombinant protein is useful for identifying  
CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
CC useful for diagnosing, treating or preventing asthma, allergy,  
CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
CC dependent diabetes mellitus, hyperglycemia, constipation, arthralgia,  
CC disorders of the neuroendocrine system, stress and spasticity

XX Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1,75e-171 Length: 1176  
Score: 2035.00 Matches: 390  
Percent Similarity: 99.74% Conservative: 0  
Best Local Similarity: 99.74% Mismatches: 1  
Query Match: 99.37% Indels: 0  
Gaps: 0

US-10-626-445-8 (1-391) x AAI70981 (1-1176)

QY 1 MetSerGluSerAnSerThrGlyIleuProProAlaIleuValProleuAlaPhe 20  
Db 1 ATGTGGAGTCTAAACATCTGCGATCTTGCCACACAGCTGCTGCTGCTGCTGCTTT 60  
QY 21 LeuMetSerSerPheAlaPheAlaIleuMetValGlyValAlaValIleuAlaPhe 40  
Db 61 TTAATGCTTCATTTGCTTGTGCTAATAGTAGTACATGCTGCTGCTGCTGCTTT 120  
QY 41 ValValAspArganLeuArgHieArgSerAsnTyrPhePheLeuAlaIleuSer 60  
Db 121 GTGGTGACAGAAACCTTAAGCATGCAAGTAATATTTTCTTAATTTGGCTAATTTCT 180  
QY 61 AspPheLeuValGlyLeuIleSerIleProleuTyrIleProHISValIleuPheAsnTyr 80  
Db 181 GACTTCTCTGGGTGATTTTCCATTCCTCTGACATCCCTCCGCTGTTTAACTGG 240  
QY 81 AsnPheGlySerGlyIleCysMetPheTyrPheuIleThrAspTyrIleuLeuCysThrAla 100  
Db 241 AATTTGGAAGTGAATCTGCATGTTTGGCTCATTAATCTGCTTTTGTGACCGCA 300  
QY 101 SerValTyrAnIleValIleuIleSerTyrAspArgTyrGlnSerValIleuAlaVal 120  
Db 301 TCGTCTACAAATATGCTCTCATTAAGTACATGATGATCAAGTTCAGATTCAAAAGCTGTG 360  
QY 121 SerTyrArgAlaGlnIleThrGlyIleMetCysIleValAlaGlnMetValAlaValTyr 140  
Db 361 TCTTTATGGGCTCAACACATGCGCATCATGAAGTTTGTGCTCAAAAGTGGCTTTGG 420  
QY 141 IleuValaPheLeuValaIleuGlyProMetIleuValaSerAspSerTyrIleuValaSer 160  
Db 421 ATACTGCTTTCTTGTAAATAGCCCATGATGCTTGGCTTCAAGTTCTTGTGAAGAAGCAGC 480  
QY 161 ThrAsnThrIleuValaPheGluProGlyPheValThrGluTyrTyrIleuThrIleThr 180  
Db 481 ACGAACAACAAGGAGCTGTGAGCTGCTTTGTTACAGAGGTGATCATCTCACCATTTACA 540

QY 181 MetLeuGluIlePheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
Db 541 ATCTCTTGAATATTCGCTTCTGTCATCTGTGGCTTATTCATATGATGACATTTAC 600  
QY 201 TyrSerLeuTyrPheArgAlaIleuSerArgCysProSerHISalGlyPheSerThr 220  
Db 601 TGGAGCTGTGGAAGGATGAGGCTTCCAGATGAGTGCCTTAAGCATCTGATTTCTCCACT 660  
QY 221 ThrSerSerSerAlaSerGlyHISLeuHISArgAlaGlyValAlaCysArgThrSerAsn 240  
Db 661 ACCCTTTCAGTCTTTCAGACACTTACACAGAGCTGGGCTGCTTCAGACAGATTAAT 720  
QY 241 ProGlyLeuValGluSerAlaIleuSerArgHISerGluSerProArgArgIleSerSer 260  
Db 721 CCGGATTTGAAGAAATCAGCTGATCTCGTCACTCAGAAAGTCTCGAAGAAGAGCAGC 780  
QY 261 IleuValaSerLeuArgThrHISMetAnSerSerIleThrAlaPheValGlySer 280  
Db 781 ATCTGGTGTCTTAAAGGACTCAATGAACAGCATGATCACTGCTTCAAAAGTGGCTTCC 840  
QY 281 PheTyrArgSerGluSerAlaIleuArgGluTyrAlaGluLeuLeuArgGly 300  
Db 841 TTTCTGGGATCGAAGAGTGCAGGCTTTCGCCAAGAGGATGACCAAGACTTCTCAAGGC 900  
QY 301 ArgLeuLeuAlaArgSerLeuAlaIleuLeuSerAlaPheAlaIleCysTyrAlaPro 320  
Db 901 AGGAAGCTGACCAAGTGCATCGGCTCATCTTGAAGGCTTTTCCATTTGCTGGCTCCA 960  
QY 321 TyrCysLeuPheThrIleValIleuSerThrTyrProArgThrGluArgPolySerVal 340  
Db 961 TACTGCTGTTCACAAATGCTCTTCAATTAATCCCAAGACGAAAGCCCAATGCTGTG 1020  
QY 341 TyrTyrSerIleAlaPheTyrPheGluIleTyrPheAsnSerPheValaAsnProPheLeuTyr 360  
Db 1021 TGGTACAGCATTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTCTTCTTCTG 1080  
QY 361 ProLeuCysHISArgArgPheGluValaPheTyrIleuValaIleuValaIleuTyr 380  
Db 1081 CTTTGTGTGACAGGCTTTCAGAAAGCTTTCGAAAGATATCTTGTGTGAACAAGCA 1140  
QY 381 ProAlaLeuSerGlnAnGlnSerValSerSer 391  
Db 1141 CCAGCGCTGTCAAGAACAGTCAATATCTTT 1173

RESULT 2  
AD030257 standard; cDNA; 1538 BP.  
ID AD030257  
AC AD030257;  
XX 29-JUL-2004 (first entry)  
DT 29-JUL-2004 (first entry)  
XX Mouse GPCR HRH4 polynucleotide, SEQ ID NO:1360.  
DE G protein-coupled receptor; GPCR; drug screening; diagnosis;  
XX transgenic mouse; neurological disorder; adrenal gland disorder;  
XX colon disorder; intestinal disorder; cardiovascular disorder;  
XX muscular disorder; blood disorder; immune disorder; bone disorder;  
XX joint disorder; metabolic disorder; nutritive disorder; cancer;  
XX kidney disorder; liver disorder; lung disorder; breast disorder;  
XX ovary disorder; uterus disorder; prostate disorder; testis disorder;  
XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
XX thymus disorder; thyroid disorder; antiparkinsonian; antineurotic;  
XX cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
XX CNS; central nervous system; respiration; antidiabetic; antidiabetic;  
XX vitamin; hepatotropic; antibacterial; antianemic; antiseborrheic;  
XX dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
XX immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
XX murine; gene; ss.  
XX Mus musculus.  
OS Mus musculus.  
XX  
XX  
PN MO2004040000-A2.

XX 13-MAY-2004.  
 PD 09-SEP-2003; 2003WO-US028226.  
 XX 09-SEP-2002; 2002US-0409303P.  
 XX PR 09-APR-2003; 2003US-0461329P.  
 XX (PRIM-) PRMAL INC.  
 XX Galanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F,  
 PI Madisen L, McIlwain XL, Pavlova MN, Vassiliadis D, Zeng H;  
 XX MPI; 2004-390329/36.  
 DR P-PSDB; ADO29497.  
 DR Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 XX  
 XX Claim 151, SEQ ID NO 1360; 542pp; English.  
 XX  
 CC The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridize to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding  
 CC nucleic acid of the invention. Note: The full sequence data for this  
 CC patent did not form part of the printed specification; those sequences  
 CC not shown were obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 1538 BP; 357 A; 362 C; 340 G; 479 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2,576-171 Length: 1538  
 Score: 2035.00 Matches: 390  
 Percent Similarity: 99.74% Conservative: 0  
 Best Local Similarity: 99.74% Mismatches: 1  
 Query Match: 99.37% Indels: 0  
 DB: 12 Gaps: 0  
 US-10-626-445-8 (1-391) x ADO30257 (1-1538)  
 QY 1 MetSerGluSerPheAlaSerThrGlyIleLeuProPheAlaGlnValProLeuAlaPhe 20  
 Db 61 ATGTGGAGTCTAAAGTAAGTGGATCTTGGCCACAGAGTGGTCCATCCCTTGGCATT 120  
 QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIleLeuAlaPhe 40

Db 121 TTAATGCTTCATTTGCTTGTATTAATGAGCAATGCTGTGTCATCTTACCTTT 180  
 QY 41 ValValaAaPaGaAaLeuAaGHaSaRgSerAntYrPhePheLeuAaLeuAlaIleSer 60  
 Db 181 GTGGTGACAGAAACCTTAGACATGAAAGTATATTTTTTTCTTAATTTGGCTATTCT 240  
 QY 61 AaPheLeuValGlyLeuIleSerIleProLeuTyrlleProHlaValLeuPheAaNTp 80  
 Db 241 GACTTCCTCGGGGTTTATTTCCATTCCTCTGACATCCCTCAGGTGTGTTTAACTCG 300  
 QY 81 AaPheGlySerGlyIleCysEwePheTrpLeuIleThraaPyrGlnLeuCyAThrAla 100  
 Db 301 AATTTGGAAAGTGAATCTGCATGTTTGGCTCATTAATGACTATCTTTGGACCCGA 360  
 QY 101 SerValTyraenIleValLeuIleSerTyraaPaGlyrGlnSerValSerAsnAlaVal 120  
 Db 361 TCTGCTCAATATATGCTCTCATTAAGTACATCATCATCATCATCATCATCATCATCAT 420  
 QY 121 SerTyraGAlaGlnHlaThGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140  
 Db 421 TCTTATAGGCTCAACACATGAGCTGATCATGAAGATTTGCTCAATATGAGCTTTGG 480  
 QY 141 IleLeuAlaPheLeuValaAsnGlyProMetIleLeuAlaSerAaPSeTrpLysAaSer 160  
 Db 481 ATACTGGCTTTCTTGTAAATGAGCCGATGATTTGCTGCTTCAAGATTTGGAAACAGC 540  
 QY 161 ThrAenTrpLysAaPSeGlyProGlyPheValThrGlyTrpTyrlleLeuThrIleThr 180  
 Db 541 ACGAACACAAAGGACATGAGACCTGGCTTTGTACAGAGTGTATATCTCACATTTTCA 600  
 QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyraPheAsnValGlnIleTy 200  
 Db 601 ATGCTCTTGAAATCT 660  
 QY 201 TrpSerLeuTrpLysAaRgAlaLeuSerAaRgCysProSerHlaAlaGlyPheSerThr 220  
 Db 661 TGGAGCTGTGGAAGCGTAGGGCTCTCATGAGTGGCTTACAGCAGATTCCTCACT 720  
 QY 221 ThrSerSerSerAlaSerGlyHlaIleuHlaBaRgAlaGlyValAlaCysAaRgThSerAsn 240  
 Db 721 ACCCTTTCAGTGTCTTACGACACTTACACAGAGCTGGGGGTGGCTTGGACGACAGTAT 780  
 QY 241 ProGlyLeuLysGluSerAlaAlaSerAaRgHlaSerGluSerProAaRgLysSerSer 260  
 Db 781 CCTGATGAAAGAAATCCGCTGATCTGTACCTAGAAAGTCTCGAAAGAAAGACAGC 840  
 QY 261 IleLeuValSerLeuAaRgThRHaEweAaSerSerIleThraAlaPheLysValGlySer 280  
 Db 841 ATCCGTGGTGTCTTAAAGACATCATGAACAGCATACATGCTTCAAGTGGCTTCC 900  
 QY 281 PheTrpAaRgSerGluSerAlaAlaLeuAaRgGlnAaRgIleTyraAlaGlnLeuLeuAaRgI 300  
 Db 901 TTCTGGCGATCGAAAGAGCGCGCTTGCAGAAAGGGAGTGCAGACCTTCTCAGAGGC 960  
 QY 301 ArgLysLeuAlaAaRgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 Db 961 AGAAGCTAGACGAGCTCATCTGCTCTTGTGAGCGCTTTGGCCATTGTGCGGCTCCA 1020  
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyraaRgTrpGluAaRgProLysSerVal 340  
 Db 1021 TACTGTCTGTTCAACATTTGCTTCAATCCCGAAGAGGAGCCCAAAATCGGGT 1080  
 QY 341 TrpTyraSerIleAlaPheTrpLeuGlnTrpPheAaSerPheValaAaPheProPheLeuTy 360  
 Db 1081 TGGTACAGCATTTGCTTGTGCTGCAATGATGTTCAATTCGTTGTTAAATCCCTTCTGTAC 1140  
 QY 361 ProLeuCySHaSaRgAaPheGlnLysAlaPheTrpLysIleLeuCyValThrIleTyra 380  
 Db 1141 CCTTGTGTCAAGGCGTTTCCAGAGGCTTTCTGAAAGATATCTTGTGTGCAAGCA 1200  
 QY 381 ProAlaLeuSerGlnAaGlnSerValSerSer 391  
 Db 1201 CCAAGCGTGTCAAGAACATCATGATATCTTCT 1233

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XX AC AA170982 standard; cDNA; 1176 BP.
XX AC AA170982
XX AC AA170982;
XX DT 18-MAR-2002 (first entry)
XX DE Rat histamine H4 receptor cDNA.
XX KM Histamine H4 receptor; rat; antiastrumatic; antiasthergenic;
XX KW antiinflammatory; cardiatic; circulatory; antidiabetic; laxative;
XX KW diagnosis; gene therapy; ss.
OS Rattus rattus.
XX WO200192485-A1.
XX PD 06-DEC-2001.
XX PF 22-FEB-2001; 2001WO-US005914.
XX PR 31-MAY-2000; 2000US-020826OP.
XX PA (ORTH ) ORTHO-MCNEIL PHARM INC.
XX PI Lovenberg T, Liu C;
XX DR WPI; 2002-114339/15.
XX PS P-PSDB; AAMS0566.
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
PS Claim 4; Fig 5C; 92pp; English.
XX The present sequence is that of a cDNA clone encoding a rat histamine
XX receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA
XX library. It shows 72.5% homology to the human H4 receptor coding region.
XX The invention provides mammalian (human, mouse, rat and guinea pig)
XX histamine H4 receptor nucleic acid molecules (see AA170980-83) and
XX polypeptides (see AAMS0564-67). The nucleic acids have been expressed in
XX recombinant host cells that produce active recombinant protein. The
XX pharmacology of known histamine ligands is demonstrated. Mammalian
XX histamine H4 receptor may be used in gene therapy for the treatment of
XX diseases where it is beneficial to elevate mammalian histamine H4
XX receptor activity. Recombinant protein is useful for identifying
XX modulators of the mammalian histamine H4 receptor. Such modulators may be
XX useful for diagnosing, treating or preventing asthma, allergy,
XX inflammation, cardiovascular and cerebrovascular disorders, non-insulin
XX dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
XX disorders of the neuroendocrine system, stress and spasticity
SQ Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1,23e-145      Length:      1176
Score:          1745.00        Matches:     332
Percent Similarity: 89.26%    Conservative: 17
Best Local Similarity: 84.91%   Mismatches:  42
Query Match:      85.21%       Indels:      0
DB:               Gaps:         0

US-10-626-445-8 (1-391) x AA170982 (1-1176)
QY      1 MetSerGluSerAsnSerThrglyIleuPProFoaAlaAlaGlnValProLeuAlaPhe 20
Dba      1 ATGTGGAGACTTAAACGGCACTGACGCTTGCCACAATGACGCTCAAGTCCCTTGGCATTT 60
QY      21 LeuMetSerSerPheAlaPheAlaIleMetValGIyAsnAlaValValIleLeuAlaPhe 40

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Db	61	TTAATGTCCTCGCTGCTTTGGCTAATAAGCATAGACAAATGCTGATGCTATTAGCCTTT	120
QY	41	ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer	60
Db	121	GTACAGACAGAAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTGGCTAATTTCT	180
QY	61	AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp	80
Db	181	GACTTCTTCGGGGGTCATCTCAATTCCTCTGTACATCCCTCAACGGCTTTTAACCTGG	240
QY	81	AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla	100
Db	241	AATTTGGAAATGGAATCGAATCGATTTTTGGCTCATTTACTACTATCTTTGTGCACAGCA	300
QY	101	SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal	120
Db	301	TCCGCTTACAGTAATGCTTCATATGCTACAGATCGAATACAGTACAGTTTCAAGCGCTGTG	360
QY	121	SerTyrTrpArgIleAsnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp	140
Db	361	CGTTATAGAGACAGCACACTGGGATCTGTAAAAATGTTGCTCAAAAGTGTCGTTTGG	420
QY	141	IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer	160
Db	421	ATACTGGCTTTCTTGCTCAATGAGGCCCAATATTTGGCTTCGGATTTCTGGAAAGACAGC	480
QY	161	ThrAsnTrpLysAspCysGlnProGlyPheValThrGluTyrIleLeuThrIleThr	180
Db	481	ACCAACACAGAGAGAGGTGGAGCCCTGGCTTGTACTAGGTGGTCAATCTCGCCATTACA	540
QY	181	MetLeuGlnIlePheLeuLeuProValIleSerPalaIleTyrPheAsnValGlnIleTyr	200
Db	541	GCATTTTGGAATTCCTGCTCCCTGCTCCTTGGTGTCTATTTCAGTACAGATTTAC	600
QY	201	TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr	220
Db	601	TGGAGCTCTGGGAAGCCTGGAGAGCTCAGTAGTGCCCTTAGCCACGCTGGATTATGCGCT	660
QY	221	ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn	240
Db	661	ACCTCTTCCAGGGGACCTGACACTGCACGCGAAGACTGGGTGGCTTGTAGCAACAGCTTT	720
QY	241	ProGlyLeuLysGlnSerAlaAlaSerArgHisSerGlnSerProArgGlySerSer	260
Db	721	CTCGATTTAAAGAACACGCCGATCCCTTATTCAGAAAGTCCACAGAGAAAGACAGT	780
QY	261	IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer	280
Db	781	CTCTCGGTGTCCTTAAGACTCACTAAGCGGTATGATCATCGCTTCAAAAGTGGTTCC	840
QY	281	PheTrpArgSerGlnSerAlaAlaLeuArgGlnArgLysTyrAlaGlyLeuLeuArgGly	300
Db	841	TTCTGCGGATCAGAAACCCAGTGCCTTCCACAGAGAGACGCGTGGAGCTTCTCAGAGGC	900
QY	301	ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro	320
Db	901	AGGAGCTAGACAGAGTGTAGCTGCTCTCTGTAGTCTTTGGCATTTTGCTGGGCTCG	960
QY	321	TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGlnArgProLysSerVal	340
Db	961	TATTGCTCTTCCAAATTTCTTTTCAACTTATGCGAGAGGGGAGGCCCCCAATTCATTT	1020
QY	341	TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr	360
Db	1021	TGGTACAGCAATAGCCTTTTGGCTCAGATGGTTCATTTACATTAATTAATCCCTTTCTATAC	1080
QY	361	ProLeuCysHisAspArgPheGlnLysAlaPheTrpLysIleLeuCysValIleThrLysTrp	380
Db	1081	CCTTTGGCCACAGACGTTTCCAAAGGCTTTTCGGAAGATACCTGTGTGACAAAGCA	1140
QY	381	ProAlaLeuSerGlnAsnGlnSerValSerSer	391
Db	1141	CCAGACACTTCACAGACCCAGTCAATCTTTCT	1173

RESULT 4  
AADS5126  
ID AADS5126 standard; DNA; 1170 BP.  
XX  
XX AADS5126;  
AC  
XX  
DT 07-AUG-2003 (first entry)  
XX  
XX Human H4 receptor wild-type DNA #2.  
DE  
XX  
XX Human; H4; histamine receptor; inflammatory bowel disease; psoriasis;  
KM atopic dermatitis; stroke; myocardial infarction; migraine; allergy;  
KM chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;  
KM rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;  
KM asthma; receptor; gene; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH 1.1170  
FT CDS /tag= a  
FT /product= "Human H4 protein"  
FT /note= "CDS does not include stop codon"  
FT /partial  
XX  
XX WO2003020907-A2.  
XX  
XX 13-MAR-2003.  
XX  
XX 30-AUG-2002; 2002WO-US027891.  
XX  
XX 31-AUG-2001; 2001US-0316762P.  
XX PR 13-NOV-2001; 2001US-0332697P.  
XX  
XX (MERI ) MERCK & CO INC.  
XX  
XX PA  
XX PI Gallagher MJ, Yates SL;  
XX  
XX WPI, 2003-290186/28.  
XX DR P-PSDB; AAE36417.  
XX  
XX Novel splice variants of human H4 histamine receptor, H4b and H4c, useful  
PT for identifying agonists or antagonists of the receptor which are useful  
PT for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.  
XX  
XX PS Disclosure; Page 56-58; 31pp; English.  
XX  
XX The invention relates to splice variants of human H4 histamine receptor,  
CC H4b and H4c. The invention is useful for identifying an agonist,  
CC antagonist or inverse agonist of a mammalian histamine receptor. The  
CC agonist, antagonist or inverse agonist of H4b and H4c is useful for  
CC treating inflammation, asthma, allergy, atopic dermatitis, stroke,  
CC myocardial infarction, migraine, chronic obstructive pulmonary disease  
CC (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel  
CC disease, or psoriasis. The present sequence is human H4 receptor DNA  
XX  
XX Sequence 1170 BP; 292 A; 245 C; 231 G; 402 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 2 916-112 Length: 1170  
Score: 1370.50 Matches: 267  
Percent Similarity: 78.32% Conservative: 40  
Best Local Similarity: 68.11% Mismatches: 82  
Query Match: 66.92% Indels: 3  
DB: 9 Gaps: 2  
US-10-626-445-8 (1-391) x AADS5126 (1-1170)  
Qy 1 MetSerGluSerAsnSerThrGlyIleuProAlaAlaGlnValProleuAlaPhe 20  
Db 1 ATGCAGATACCTAATAGCACATCAATTTATCATCAGACATCGGTGTACTTACATTT 60

Qy 21 LeuMetSerSerPheAlaPheAlaIleuMetValGlyAsnAlaValAlaIleuAlaPhe 40  
Db 61 TTTATGTCCTTAGTACGCTTTTCTTATATGCTAGGAATGCTTGTGCTATTTAGCTTTT 120  
Qy 41 ValValaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 121 GTGGTGACAAAGAACCTTAGACATGAGTAGTATTTTCTTAACTTGGCCATCTCT 180  
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80  
Db 181 GACTTCCTTGTGGGTGATGCTCCATTCCTTGTGACATCCCTCACACCGCTTGCATAGG 240  
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleTrpAspTyrLeuLeuCysThrAla 100  
Db 241 GATTTGGAGGAAGAAATCTGTATTTGGCTCCTACTGACTGACTGCTTATATGTCAGCA 300  
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
Db 301 TCTGTATATTAACATTTGCTCTCATGCTATGATGATGATGCTGCTCAATGCTGTG 360  
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTrp 140  
Db 361 TCTTATAGAACTCAACATACCTGGGCTTGAAGATTGACTCTGATGCTGCTGCTTGG 420  
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160  
Db 421 GTGCTGGCCCTTTAGTAAATGGCCAAATGATTTAGTTTCAAGACTTGGAGGAATGAA 480  
Qy 161 ThrAsnThrIleAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180  
Db 481 GGTACT-----GAATGGAACTGTGATTTTTCGAATGGTATCATCTTCCATCACA 534  
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
Db 535 TCATTCCTTGAATTCGATCCAGTCCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594  
Qy 201 TrpSerLeuTrpIleArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
Db 595 TGGAGCCGTGGAGCGATCATCATCTCAGTAGAGTCCAAAGCATCTGGAGCTGACTCT 654  
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
Db 655 GTCCTTCCAACTGTGGACATCTCAGACATCTCAGAGTAGACTTCCAAAGAGATCTCT 714  
Qy 241 ProGlyLeuValGluSerAlaAlaSerArgHisSerGluSerProArgArgIleSerSer 260  
Db 715 TCTGCATCAGACAAAGTTCTCTCATCTTATCATTAGAGACACAGAGAAAGAGTAGT 774  
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheValGlySer 280  
Db 775 CTCATGTTTCTCTCAAGAACCAAGATGAATGCAATCAATGCTTCCAAATAGGCTTCC 834  
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgIleTyrAlaGlyLeuLeuArgGly 300  
Db 835 TTCTCCCAATCAGATCTCTAGCTTTCACCAAGAGCAATGTGAATCTGTTAGAGCC 894  
Qy 301 ArgIleLeuValArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
Db 895 AGAGATATAGCCAAATGCTGCGCATCTCTTAGGGGTTTGTGCTGTGCTGCGCTCCA 954  
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProIleSerVal 340  
Db 955 TATTTCTGTTCCACATTTGCTTTTCATTTATTCCTCAGCAACAGGCTCTTAATCAGTT 1014  
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360  
Db 1015 TGTATATAGATTTGCTTTGCTTCAAGTGTTCATCTTGTGCAATCCTCTTTTGTAT 1074  
Qy 361 ProLeuCysHisArgArgPheGlnIleValAlaPheTrpIleValLeuCysValThrIleTyr 380  
Db 1075 CCATTTGTCTCACAAGCCGCTTTCAAAGGCTTTCGAAATATTTTGTATATAAAGCA 1134  
Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391

DB 1135 CCTTACATCACAACAGTCGTCAGTATCTTCT 1170  
RESULT 5  
ID AAA46023 standard; cDNA; 1173 BP.  
AC AAA46023;  
XX 22-AUG-2000 (first entry)  
XX Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13.  
XX Human; G protein coupled receptor; GPCR; transmembrane receptor;  
XX Identification; agonist; screening; therapeutic; pharmaceutical; mutant;  
XX ss.  
XX Homo sapiens.  
XX MO200022131-A2.  
XX 20-APR-2000.  
XX 13-OCT-1999; 99MO-US024065.  
XX 13-OCT-1998; 98US-00170496.  
XX 12-NOV-1998; 98US-0108029P.  
XX 20-NOV-1998; 98US-0109213P.  
XX 27-NOV-1998; 98US-0110060P.  
XX 16-FEB-1999; 99US-0120416P.  
XX 26-FEB-1999; 99US-0121852P.  
XX 12-MAR-1999; 99US-0123944P.  
XX 12-MAR-1999; 99US-0123945P.  
XX 12-MAR-1999; 99US-0123946P.  
XX 12-MAR-1999; 99US-0123948P.  
XX 12-MAR-1999; 99US-0123949P.  
XX 12-MAR-1999; 99US-0123951P.  
XX 28-MAY-1999; 99US-0136437P.  
XX 28-MAY-1999; 99US-0136437P.  
XX 28-MAY-1999; 99US-0136439P.  
XX 28-MAY-1999; 99US-0137127P.  
XX 28-MAY-1999; 99US-0137131P.  
XX 28-MAY-1999; 99US-0137567P.  
XX 29-JUN-1999; 99US-0141448P.  
XX 27-AUG-1999; 99US-0151114P.  
XX 03-SEP-1999; 99US-0152524P.  
XX 29-SEP-1999; 99US-0156555P.  
XX 29-SEP-1999; 99US-0156633P.  
XX 29-SEP-1999; 99US-0156634P.  
XX 29-SEP-1999; 99US-0156635P.  
XX 01-OCT-1999; 99US-0157280P.  
XX 01-OCT-1999; 99US-0157281P.  
XX 01-OCT-1999; 99US-0157282P.  
XX 01-OCT-1999; 99US-0157283P.  
XX 01-OCT-1999; 99US-0157294P.  
XX 12-OCT-1999; 99US-00416760.  
XX 12-OCT-1999; 99US-00417044.  
XX (AREN-) ARENA PHARM INC.  
XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT,  
XX Gore M, Liaw CW, Lin I, Lowitz K, White C;  
XX WPI; 2000-317986/27.  
XX P-PSDB; AAB02831.  
XX Non-endogenous, human G protein-coupled receptors for screening receptor,  
XX inverse or partial agonists useful as therapeutic agents.  
XX Example 1; Page 88-89; 187pp; English.  
XX The present invention describes transmembrane receptors, preferably human  
XX G protein coupled receptors (GPCR), for which the endogenous ligand is

CC unknown (orphan GPCR receptors). More specifically the present invention  
CC relates to non-endogenous, constitutively activated versions of a human  
CC GPCR. These non-endogenous human GPCRs can be useful for the direct  
CC identification of candidate compounds as receptors agonists, inverse  
CC agonists or partial agonists for use as pharmaceutical agents. AAA46017  
CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 2,92e-112 Length: 1173  
Score: 1370.50 Matches: 267  
Percent Similarity: 78.32% Conservative: 40  
Best Local Similarity: 68.11% Mismatches: 82  
Query Match: 66.92% Indels: 3  
DB: 3 Gaps: 2  
US-10-626-445-8 (1-391) x AAA46023 (1-1173)  
Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20  
Db 1 ATCCGATGATCTAATAGCACAATCAATTTATCTACAGCACTGCTTACTTATGACATTT 60  
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40  
Db 61 TTTATGCTCTTACTTACTTCTTATATGCTGAAATGCTTGTGCTCATTTTATGCTTTT 120  
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuLeuAlaIleSer 60  
Db 121 GTGTGGACAAAACCTTAGACATGCAAGAGTATTTTCTTAACTGGCACTCT 180  
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80  
Db 181 GACTTCTTGTGGGTGGATGATCTCATTTCTTTATCATCCCTCACAGCGTTGCAATGG 240  
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
Db 241 GATTTTGAAAGAAATCTGTATTTGGCTCACACTGACATCTGTTATGTACAGCA 300  
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGluSerValSerAsnAlaVal 120  
Db 301 TCTGTATATACATGCTCCATCAGCTAGTGAATGCTGCTGCTCAATGCTG 360  
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetValIleValAlaGlnMetValAlaTyr 140  
Db 361 TCTTATGAACTCAACATCACTGGGCTTGAATTTTACTGATGGTGGCGTTGG 420  
Qy 141 IleLeuAlaPheLeuValLeuGlyPrometIleLeuAlaSerAspSerTyrPheAsnSer 160  
Db 421 GTCTGGCCTTCTTATGAAATGGGCCAATGATTTCTAGTTCAAGATCTTGGAAAGATGAA 480  
Qy 161 ThrAsnThrIleAspCysGluProGlyPheValThrGlnTyrPheIleLeuThrIleThr 180  
Db 481 GGTAAGT-----GAATGTGAACCTGGAATTTTTCGAAAGTGAACATCTTGGCATCACA 544  
Qy 181 MetLeuGluGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
Db 545 TCATTTCTGGAATTCGTGATCCCACTCATCTTATGCTTATTTCAACATGATATTAT 564  
Qy 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
Db 565 TGAGCCTGTGCAAGCGTATCATCTCAGTAGGTCGCAAGCATCTCGGACATGACGTCT 654  
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaLacysArgThrSerAsn 240  
Db 655 GTCTCTTCAAACTCTGTGACACTGATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714  
Qy 241 ProGlyLeuValGluSerAlaSerArgHisArgSerAsnTyrPhePheLeuLeuAlaIleSer 260  
Db 715 TCTGCATTCACAGAAAGTCTCTGATCTTCTTCACTTACAGAGACAGAGAAAGAGTACT 774  
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheValGlySer 280











CC the detection of mutations in the corresponding gene. AXOR35 proteins are  
 CC also useful for inducing an immunological response in a mammal against  
 CC the above diseases, and for antibody production. AXOR35 nucleotides are  
 CC also useful as diagnostic reagents, in chromosome localisation and tissue  
 CC expression studies, and for producing transgenic animals useful in drug  
 CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35  
 CC protein or fragments thereof, and are also useful for treating conditions  
 CC associated with the expression of the AXOR35 protein. The present  
 CC sequence represents cDNA encoding human AXOR35

XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	2,92e-112	Length:	1173
Score:	1370.50	Matches:	267
Percent Similarity:	78.32%	Conservative:	40
Best Local Similarity:	68.11%	Mismatches:	82
Query Match:	66.92%	Indels:	3
DB:	5	Gaps:	2

US-10-626-445-8 (1-391) x AAH24007 (1-1173)

QY 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaIleValIlePheValIlePhe 20  
 DB 1 ATGCCAGTACTATATACCAATCAATTTATCACTAGCACTCTCGTTACTTTAGCATTT 60  
 QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40  
 DB 61 TTTATGCTCTTAGTAGCTTTTGTCTATATAGTAAATGCTTTGGTCATTTTAGCTTTT 120  
 QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 DB 121 GTGGTGACAAAACCTTAGCATCGAAGTAGTATTATTTTCTTAACTGGCCATCTCT 180  
 QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIlePheAsnTyr 80  
 DB 181 GACTTCTTGTGGTGATCTCCATTCCTTTGTACATCCCTCAACGCTGTCGAATGG 240  
 QY 81 AspPheGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrIleLeuAsnCysThrAla 100  
 DB 241 GATTTTGGAAAGAAATCTGTATTTTGGCTCACTAGCTACTATCTGTATGTACGCA 300  
 QY 101 SerValTyrAsnIleValIleLeuIleSerTyrAspArgTyrGlnSerValIleAsnAlaVal 120  
 DB 301 TCGTATATATAACATTCCTCATCAGCTATGATGATACCGTCACTCAAAATGCTGTG 360  
 QY 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140  
 DB 361 TCTTATAGAACTCAACATCTAGGCGGTCTTGAAGATTTCTTACTGTGATGGCCGTTTG 420  
 QY 141 IleLeuAlaPheLeuValIleAsnGlyIleProMetIleLeuAlaIleSerAspSerTyrPheAsnSer 160  
 DB 421 GTGCTGCTCTTCTTGAATGGCCATGATGATTTTCAAGATCTTGAAGAGATGAA 480  
 QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180  
 DB 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGAAATGTATCATCTTGGCATCACA 534  
 QY 181 MetLeuLeuGlnPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
 DB 535 TCATTTCTTGGAAATTCGATCCCAAGTATCTTATCTCTTATTTCAACATGAATATTAT 594  
 QY 201 TyrSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyIlePheSerThr 220  
 DB 595 TGAAGCTGTGGAAAGCTGATCATCTCAGTAGTGCCAAAGCCATCTGGATGACACTCT 654  
 QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgHisAlaGlyIleValAlaCysArgThrSerAsn 240  
 DB 655 GTCTCTTTCGAACAATCTGTGACACTCATTCAGAGTAGACTATCTTCAAGAGATCTCTT 714  
 QY 241 ProGlyLeuLysGluSerAlaIleSerArgHisIleSerGluSerProArgTargLysSerSer 260  
 DB 715 TCTGCATCGACAGAAATTCCTGCATCTTTCATTCAGAGAGACAGAGAGAAAGATAGT 774

QY 261 IleLeuValSerLeuArgThrHisMetAsnSerIleThrAlaPheLysValGlySer 280  
 DB 775 CTCATGTTTCTCCAGAACCAAGATGAATAGCAATATTCCTCCAAATAGGGTTC 834  
 QY 281 PheTyrArgSerGluSerAlaAlaLeuArgGlnArgGlyTyrAlaGluLeuValGly 300  
 DB 835 TTCTCCCAATCAGATTCGTAGCTCTTACCAAGGGAACATGTGAATCGTTAGAGCC 894  
 QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTyrPheAlaPro 320  
 DB 895 AGGAGATTAGCCAGATCAGCGCATTCCTTAGGGGTTTCTGTTGCTGGCCCA 954  
 QY 321 TyrCysLeuPheThrIleValIleSerThrTyrProArgThrGluArgProLysSerVal 340  
 DB 955 TATTCCTGTTCCACATTCGTCTTATTTATTCAGCAACAGGCTTAATACAGTT 1014  
 QY 341 TyrTyrSerIleAlaPheTyrPheGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360  
 DB 1015 TGGTATAGAAATTCATTTGGCTTCAAGTGGTCAATTCCTTGTCAATCCTCTTTGTAT 1074  
 QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTyrPheIleLeuCysValThrLysTyr 380  
 DB 1075 CCATGTGTCACAAAGGCTTCAAAAGCTTTCTTGAAATATTTGTATAAAAAGCAA 1134  
 QY 381 ProAlaLeuSerGln--AeGlnSerValSerSer 391  
 DB 1135 CCTTACCATCACAACAACAGTGGTCAATCTCTT 1170

RESULT 9  
 ABZ80663 standard; cDNA; 1173 BP.  
 ABZ80663;  
 AC  
 XX  
 XX  
 DT 13-JUN-2003 (first entry)  
 XX  
 DE Human histamine receptor coding sequence.  
 XX  
 KW human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;  
 KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;  
 KW anti-migraine; cardiant; anti-rheumatic; anti-arthritic; antipsoriatic;  
 KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;  
 KW myocardial infarction; migraine; chronic obstructive pulmonary disease;  
 KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;  
 KW psoriasis; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1173  
 FT /tag= a  
 FT /product= "Histamine receptor"  
 FT  
 XX  
 PN US6204017-B1.  
 PD 20-MAR-2001.  
 XX  
 PF 07-OCT-1999; 99US-00414010.  
 XX  
 PR 07-OCT-1999; 99US-00414010.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 PI Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP,  
 PI Wang S;  
 XX  
 DR WPI; 2002-442063/47.  
 DR P-PSDB; AB098629.  
 XX  
 PT New nucleic acid encoding antigenic part of human histamine receptor,  
 PT useful for preparing antibodies, e.g. for treating-histamine related  
 PT disorders.

PS Example 1; Col 27-28; 19pp; English.

This sequence represents the open reading frame for a human histamine receptor (HR) designated SP914. The sequence was isolated by searching databases with the sequence of known G-coupled protein receptor (GPCR). The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunoprecipitation chromatography, in immunosay of histamine receptor, to identify cDNA clones that express the receptor, as antagonist to block binding of histamine (for treating any histamine-associated disorder) and to generate anti-idiotypic antibodies. Agonists and antagonists of the HR protein can be used in the treatment of e.g. inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis

SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

**Alignment Scores:**

Pred. No.:	2,92e-112	length:	117
Score:	1370.0	Matches:	267
Percent Similarity:	78.32%	Conservative:	40
Best Local Similarity:	68.11%	Mismatches:	82
Query Match:	66.92%	Indels:	3
DB:	6	Gaps:	2

US-10-626-445-8 (1-391) X ABZ80663 (1-1173)

Qy	MeSerCyluSerXamSerTrgIylIeLeuProColAlaGlnValProLeuAlaPhe	20
Db	1 ATGCCAGATATCTAATGACACATCAATTTATCATTAGACATCGTGTACTTTAGCATTT	60
Qy	21 LeuMeSerSerPheAlaPheAlaIleMetValGlyAmaAlaValIleLeuAlaPhe	40
Db	61 TTATATGCTTACTAGTACTTTTGCTTAATAGCTAGGAATGCTTTGGTCAATTTAGCTTTT	120
Qy	41 ValValAspArgAmIeuaRghIaSaGSerAmYrPhePheLeuAmIeAlaIleSer	60
Db	121 GTGGTGGACAAAACCTTGAACATCGAATAGTATTATTTTCTTAACCTGGACATCTCT	180
Qy	61 AspPheLeuValGlyLeuIleSerIleProLeuYrIleProHValIlePheAsnTrp	80
Db	181 GACTTCTTTGTGGGTGTGATCTTCATCTCTTTGTACATCCCTCACACCTGTGTGATGG	240
Qy	81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspYrLeuLeuCysThrAla	100
Db	241 GATTTTGGAAGGAATCTGTGTATTGTCCTGACCTAGTACTATCTTTATGACAGCA	300
Qy	101 SerValTyrAsnIleValLeuIleSerYrAspArgYrTrgIleSerValSerPheAlaVal	120
Db	301 TCTGATATATACATGTGCTTCATACACTATGATACATCTGTCACTGTCATTAAGTCTGTG	360
Qy	121 SerTyrArgIaGlnIleThrGlyIleMetCylIleValAlaGlnMetValAlaValTrp	140
Db	361 TCTTATATGAACCTCAACATACCTGGGGCTTGAAAGATTGTTACGTGATGTGGCGGTTTGG	420
Qy	141 IleLeuAlaPheLeuValIeAngIyProMetIleLeuAlaSerAspSerTrpIleAsnSer	160
Db	421 GTCTGGCCCTTCTTATGTGAATGGCCAAAGATTCTAGTTCAGACTCTTGGAGAGATGAA	480
Qy	161 ThrAsnThrIlyAspPheCysGluProGlyPheValIleTrgIuTrpYrIleLeuThrIleThr	180
Db	481 GGATGT-----GAATGTAACTGTGATTTTGTGGAAATGTACATCTTGGCATCA	534
Qy	181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaIlyrPheAsnValGlnIleYr	200
Db	535 TCATTTCTTGGAATTCGTGATCCAGATCACTTAGTGTCTTATTTCAACATGAATATTAT	594
Qy	201 TrpSerLeuTrpIlyValArgAlaIleuSerArgCysProSerHleAlaGlyPheSerThr	220
Db	595 TGAAGCTGTGGAGGATGATCATCTCATATAGATGCCAAAGCATCTGGAGTACGACT	654

QY	221	ThrsSerSerSerLaSerSerGlyHisLeuHisArgGAlaGlyValAlaCysArgTrpSerAsn	240
Db	655	GTCTTTCCACACATCTGTGGACACTCATTCCAGAGGTAGACTATCTTCACCAAGAGATCTCTT	714
QY	241	ProGlyLeuGlyGluSerAlaAlaSerArgHisSerGluSerProArgArglySerSer	260
Db	715	TCTGCATCGACAGAGAGTTCTCTGCATCTCTTCATTCAGAGAGACAGAGGAGAAAGTAGT	774
QY	261	IleLeuValSerLeuArgThrHisMetLeuSerSerIleThrAlaPheLeuValGlySer	280
Db	775	CTCATGTTTCTCTCAAGAACCAAGATGATAGCAATACATTGCTTCCAAAATGGGCTCC	834
QY	281	PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGlnIuTrpAlaGluLeuLeuArgGly	300
Db	835	TTCTCCCAATCAGATTCTGTAGCTCTTCAACCAAGGAAACATGTTGAACTGCTTAGAGCC	894
QY	301	ArglyLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCyetrpAlaPro	320
Db	895	AGAGATTAGCCAAATCACTGCGCATTTCTCTTAGGGGTTTTTGCTGTTTGCTGGGCTCCA	954
QY	321	TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProIlySerVal	340
Db	955	TATTCCTGTTCCACAATGTCCTTTCATTATTCCTCAGCAACAGTCTCTAATCAGTT	1011
QY	341	TrpTyrSerIleAlaPheTrpLeuGlnTrpPheLeuSerPheValAspProPheLeuTyr	360
Db	1015	TGGATAGAAATGGCAATTTGGCTTCAGGTTCAAATCTCTTGCAATCTCTTTTGTAAT	107
QY	361	ProLeuCyHisArgArgPheGlnIlyValaPheTrpIlyIleLeuCyValThrIlyStrp	380
Db	1075	CCATTGTGTCCACAGCGCTTTCCAAAGGCTTCTTGAAATATTTTGTATATAAANAAGCAA	113
QY	381	ProAlaLeuSerGln--AsnGlnSerValSerSer	391
Db	1135	CCTCACCATCACAACACAGCTGCGTCACTATCTTCT	1170
RESULT 10			
ABQ78739			
ID	ABQ78739	standard; DNA; 1173 BP.	
AC			
XX	ABQ78739;		
XX			
DT	05-DEC-2002	(first entry)	
DE			
XX			
DE		Nucleotide sequence of human histamine receptor.	
KW		Human; histamine receptor; receptor; inflammation; asthma; allergy;	
KW		chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;	
KW		multiple sclerosis; inflammatory bowel disease; psoriasis;	
KM		intracellular second messenger pathway; cellular growth rate;	
KW		hormone secretion; gene; ss.	
XX			
OS		Homo sapiens.	
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..1173	
FT		/*tag= a	
FT		/product= "histamine receptor"	
XX			
XX	US2002098539-A1.		
XX			
XX	25-JUL-2002.		
XX			
XX	19-MAR-2001; 2001US-00812216.		
XX			
PR	07-OCT-1999; 99US-00414010.		
XX			
PA	(BEHA/) BEHAN J X.		
PA	(HEDR/) HEDRICK J A.		
PA	(LAZT/) LAZ T M.		
PA	(MONS/) MONSMA F J.		
PA	(MORS/) MORS K L.		

PA (UMLA/) UMLAND S P.  
 PA (WANG/) WANG S.  
 PI Behan JX, Hedrick JA, Laz TM, Monema FT, Morse KL, Umland SP;  
 PI Wang S;  
 XX WPI; 2002-673827/72.  
 DR P-PSDB; ABB78276.  
 XX Novel mammalian histamine receptor polypeptide useful for identifying  
 PT agonist or antagonist for treating diseases such as inflammation, asthma,  
 PT stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.  
 XX  
 PS Example 1; Page 15-16; 21pp; English.

CC The present sequence encodes a human histamine receptor. The polypeptide  
 CC is useful for identifying an agonist or antagonist of a mammalian  
 CC histamine receptor. It is useful as an antigen to elicit the production  
 CC of antibodies. The histamine receptor polypeptide and polynucleotide are  
 CC useful in the treatment and management of diseases such as inflammation,  
 CC asthma, allergy, atopic dermatitis, stroke, myocardial infection,  
 CC migraine, chronic obstructive pulmonary disease (COPD), rheumatoid  
 CC arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.  
 CC They are also useful for modulating intracellular second messenger  
 CC pathway activated through histamine receptors (cyclic-AMP, calcium,  
 CC inositol phosphate and mitogen activated protein (MAP) kinase), changes  
 CC in cellular growth rate, secretion of hormones, receptor-stimulated Ca<sup>2+</sup>  
 CC mobilization, mitogenic effects, etc

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 2,92e-112 Length: 1173  
 Score: 1370.50 Matches: 267  
 Percent Similarity: 78.32% Conservative: 40  
 Best Local Similarity: 68.11% Mismatches: 82  
 Query Match: 66.92% Indels: 3  
 DB: 6 Gaps: 2

US-10-626-445-8 (1-391) x ABQ78739 (1-1173)

QY 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20  
 DB 1 ATGCGAGATACCTATAGCACATCAATTCATCACTAATTCCTTACTTATGACATTT 60  
 QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyValAlaValIleLeuAlaPhe 40  
 DB 61 TTTATGCTCTTAGTAGCTTTTGTCTATATAGCTAGAAATGCTTTGGTCATTTTAGCTTTT 120  
 QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAlaAlaIleSer 60  
 DB 121 GTGGTGACAAACAACTTAGACATCGAAGTAGATATTTTCTTAACTGGCCATCTCT 180  
 QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80  
 DB 181 GACTTCTTTGTGGGTGATCTCATTCCTTTGTACATCCCTCACAGCGTGTGAAATGG 240  
 QY 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIlePheAspTyrLeuLeuCysThrAla 100  
 DB 241 GATTTTGGAAGAAACCTGTGATTTTGGCTCACTAGCTATCTGTTATGTACAGCA 300  
 QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 301 TCTGTATATAACTTGTCTCATCATGATGATGATGATGATGATGATGATGATGATG 360  
 QY 121 SerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTyr 140  
 DB 361 TCTTATGAACTCAACATCTGCGGCTCTTGAAGATTTTACTGATGATGATGCGCTTGG 420  
 QY 141 IleLeuAlaPheLeuValaGlnGlyProMetIleLeuAlaSerAspSerTyrPheAsnSer 160  
 DB 421 GTCTGCGCTTCTTAGTGAATGGCCCAATATCTAGTTTCAAGTCTTGAAGAGATGAA 480

QY 161 ThrAsnThrLysAspCysGlnProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180  
 DB 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAAATGTATACATCTTGCATCACA 534  
 QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
 DB 535 TCAATTCCTGGAAATTCGTGATCCGATCATCTTGTAGTGTCTTATTTCAACATGAATATTAT 594  
 QY 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
 DB 595 TGAAGCTGTGGAAGCGTATCATCTCAGTAGGTGCAAGCAAGCATCTGATCAGTCTGCT 654  
 QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
 DB 655 GTCTCTTCCAAACATCTGTGATCCGATCATCTCAGTAGTACTATCTTCAAGATCATCTT 714  
 QY 241 ProGlyLeuLeuSerGlnAlaIleSerArgHisSerGluSerProArgArgLysSerSer 260  
 DB 715 TCTGCAATCGACAGAACTCTGATCTTTCATTCAGAGAGACAGAGAGAGAAAGATAGT 774  
 QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280  
 DB 775 CTCAATGTTTCTCCAGAACCAAGATGATGATGATGATGATGATGATGATGATGATG 834  
 QY 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300  
 DB 835 TTCTCCCAATCAGATCTGTGATCTTTCACCAAGGAAAGGAAATGTGAATCGCTTAGAGCC 894  
 QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 DB 895 AGGAGATTCAGCAAGCATCGGCTTCTTGTGGGGTCTTGTCTGTGTGCTGGCTCCA 954  
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340  
 DB 955 TATTCCTGTTCACATTCCTTCTTATTTATCTCCACAGCAACAGTCTTAATATGATT 1014  
 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360  
 DB 1015 TGGTATATGAATTCATTTTGGCTTTCAGTGGTTCATTTCTTGTCAATCTCTTGTGAT 1074  
 QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValIleThrLysTrp 380  
 DB 1075 CCAATGTGTCAACAGGCTTTCAAAAGGCTTTCTTGAATAATTTGTATATAAAGCAA 1134  
 QY 381 ProAlaLeuSerGln--AsnGlnSerValSerSer 391  
 DB 1135 CCTTACCATCACACACACAGCTCGTACGATCTTCT 1170

RESULT 11  
 AA170980 ID AA170980 standard; cDNA, 1173 BP.  
 AC AA170980;  
 XX 18-MAR-2002 (first entry)  
 DT XX  
 XX Human histamine H4 receptor cDNA.  
 DE  
 KW Histamine H4 receptor; human; antiasthmatic; antiallergenic;  
 KW anti-inflammatory; cardiac; circulatory; antidiabetic; laxative;  
 KW diagnosis; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN M02001.92485-A1.  
 XX  
 XX 06-DEC-2001.  
 PD  
 XX  
 XX 22-FEB-2001; 2001MO-US005914.  
 PF  
 XX 31-MAY-2000; 2000US-0208260P.  
 PR  
 XX  
 XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Lovenberg T, Liu C;  
 XX WPI; 2002-114339/15.  
 DR P-PSDB; AAM50564.  
 XX  
 XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX  
 PS Claim 4, Fig 1, 92pp; English.  
 XX  
 XX The present sequence is that of cDNA clone pH4R encoding a human  
 CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone  
 CC marrow cDNA library. The invention provides mammalian (human, mouse, rat  
 CC and guinea pig) histamine H4 receptor nucleic acid molecules (see  
 CC AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have  
 CC been expressed in recombinant host cells that produce active recombinant  
 CC protein. The pharmacology of known histamine ligands is demonstrated.  
 CC Mammalian histamine H4 receptor may be used in gene therapy for the  
 CC treatment of diseases where it is beneficial to elevate mammalian  
 CC histamine H4 receptor activity. Recombinant protein is useful for  
 CC identifying modulators of the human histamine H4 receptor. Such  
 CC modulators may be useful for diagnosing, treating or preventing asthma,  
 CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-  
 CC insulin dependent diabetes mellitus, hyperglycemia, constipation,  
 CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity  
 XX  
 XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 SO  
 Alignment Scores:  
 Pred. No.: 2, 926-112 Length: 1173  
 Score: 1370.50 Matches: 267  
 Percent Similarity: 78.32% Conservative: 40  
 Best Local Similarity: 68.11% Mismatches: 82  
 Query Match: 66.92% Indels: 3  
 Gaps: 2  
 DB: 6  
 US-10-626-445-8 (1-391) x AAI70980 (1-1173)  
 QY 1 MetSerGluSerAsnSerThrGlyLeuProProAlaAlaGlnValProLeuAlaPhe 20  
 DB 1 ATGCAGATCTACTATAGCAGATCAATTCATTCACAGACGCGTTACTTACGATTT 60  
 QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIleLeuAlaPhe 40  
 DB 61 TTTATGCTCTTAGTAGCTTCTTCTATATGCTGAAAGCTTGTGCTATTAGCTTTT 120  
 QY 41 ValValaAPARgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 DB 121 GTGGTGACAAACCTTAGACATGAGATGATTATTTTCTTAACCTTGCCCAATCTT 180  
 QY 61 AsPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80  
 DB 181 GACTTCTTTGTGGGTGATCTCCATTCCTTTGTATCATCCCAACGCGTGTCCAAATG 240  
 QY 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleLeuCysThrAla 100  
 DB 241 GATTTGGAAAGGAATCTGTGATTTGGCTCAGTACTGACTATCTGTTATGTCAGCA 300  
 QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 301 TCTGTATATTAACATGCTCTCATTCAGCTATGATCAATCTGCAATCTGCTGCTG 360  
 QY 121 SerTyrAsnAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTyr 140  
 DB 361 TCTTATAGAACTCAACATCTGCGGCTTGAAGATTTGTTACTGATGCTGCGCTTTGG 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIlyAsnSer 160  
 DB 421 GTGCTGGCTCTTCTGTGATGAGGCAATGATTTAGATTGAGAGTCTTGAAGATGAA 480  
 QY 161 ThrAsnThrIlyAspCysGlnProGlyPheValThrGlnTyrTrpTyrIleLeuThrIleThr 180

DB 481 GGTACT-----GAAATGCACTGGATTTTTCGGAAATGGATACCTTGCATCACA 534  
 QY 181 MetLeuLeuGluPheLeuProValIleSerValAlaIleTyrPheAsnValGlnIleTyr 200  
 DB 535 TCATTTCTGGAAATGCTGATCCAGTCACTTAGTCGCTTATTTCAACATGATATTTAT 594  
 QY 201 TPSPSerLeuTrpIlyAsnArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
 DB 595 TGGAGCTGTGGAAGCGTATCATCTCAGTAGTCCAAAGCATCTTGAGCTGACTGCT 654  
 QY 221 ThrSerSerSerAlaSerGlyHisIleuHisArgAlaGlnValAlaCysArgThrSerAsn 240  
 DB 655 GCTCTTCCAAATCTGTGGACATCTCAGATTCATCAGATGATCTTCAAGAGATCTCT 714  
 QY 241 ProGlyLeuValGluSerAlaAlaSerArgHisSerGluSerProArgArgIlySerSer 260  
 DB 715 TCTGCATCGACAGAAAGTTCTTCATCTTTCATTCAGAGAGACAGAGGAGAAAGTAGT 774  
 QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheIlyValGlySer 280  
 DB 775 CTCATGTTTCTTCAAGAAACCAAGATGATGATCAATTCATTCCTCAAAATGGATTTC 834  
 QY 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300  
 DB 835 TTCTCCCAATCAGATCTCTGATCTTTCACCAAGAGAAATCTGGAATCTTGATGAGCC 894  
 QY 301 ArgIlyLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 DB 895 AGGAGATTAGGCAAGTCACTGGCCATTCCTTAGGGGTTTGTGCTGTTGCTGGCTCCA 954  
 QY 321 TyrCysIleuPheThrIleValLeuSerThrTyrProArgThrGlnArgProIlySerVal 340  
 DB 955 TATTCTGTGTCACAAATGCTTTCATTTATTCCTCAGCAACAGGTCCTTAATCAGTT 1014  
 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360  
 DB 1015 TGGTATAGAAATGCAATTTGGCTTCAAGTGTTCATTCCTTTGTCAATCTCTTTTGTAT 1074  
 QY 361 ProLeuCysHisArgArgPheGlnIlyAlaPheTrpIlyValIleLeuCysValThrIlyTrp 380  
 DB 1075 CCATTTGTGTCACAAAGCGCTTTCAAAGGCTTCTTGAAGATTTTGTATATAAAGCAA 1134  
 QY 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391  
 DB 1135 CCTTACCATCAACAACAGTCGTGATTCCTTCT 1170  
 RESULT 12  
 ID AAI67750 standard; cDNA, 1173 BP.  
 AC AAI67750;  
 DT 27-PEB-2002 (first entry)  
 XX  
 XX Human histamine H4 receptor protein encoding cDNA.  
 XX  
 XX Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive;  
 KW antiaesthetic; antiallergic; neuroprotective; antidiabetic; human;  
 KW cerebroprotective; CAMP modulator; gene therapy; ss.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT 1..1173  
 FT CDS /tag=a  
 FT /product="histamine H4 receptor"  
 XX  
 XX W0200185786-A2.  
 XX  
 XX 15-NOV-2001.  
 XX  
 XX 04-MAY-2001; 2001WO-US014527.



XX 05-MAY-2000; 2000US-0202151P.  
 PR 23-AUG-2000; 2000US-0227567P.  
 PR 13-NOV-2000; 2000US-0247855P.  
 XX (AMHP ) AMERICAN HOME PROD CORP.  
 PA Jones PG, Blatcher M, Wu S, Pauech MH;  
 PI WPI; 2002-049442/06.  
 XX P-PSDB; AAG66023.  
 DR  
 XX  
 PT New histamine receptor, termed H4 useful for detecting H4 (ant)agonists  
 PT for treating transplanted organ rejection, asthma, allergy, multiple  
 PT sclerosis and rheumatoid arthritis.  
 XX  
 PS Claim 13; Fig 1; 66pp; English.  
 XX  
 CC The invention provides an isolated histamine receptor, H4, which binds  
 CC ligands comprising imidazole attached to amine by an alkyl chain. The H4  
 CC receptor can be expressed by standard recombinant methodology. Cells  
 CC expressing H4 receptor protein at a detectable level can suppress cyclic  
 CC adenosine monophosphate (cAMP) formation when contacted with the H4  
 CC receptor agonist. The H4 receptor and antibodies are used for identifying  
 CC H4 receptor modulators. Modulation of histamine H4 receptors is useful  
 CC for treating transplanted organ rejection, asthma, allergies and  
 CC autoimmune pathologies such as multiple sclerosis, type I diabetes,  
 CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor  
 CC protein and nucleic acids are useful targets to identify drugs that are  
 CC effective in treating disorders associated with histamine-regulated  
 CC processes. Identification and isolation of H4 receptor provides for  
 CC development of screening of molecules that interact with H4 receptors.  
 CC Genetic variants of H4 can be used to diagnose an H4 associated disease  
 CC as described above. The H4 receptor polynucleotide is useful to treat or  
 CC prevent a disorder associated with the function of H4 in peripheral blood  
 CC leukocytes. The present sequence represents a cDNA encoding the human  
 CC histamine H4 receptor protein  
 XX  
 SQ Sequence 1173 BP; 296 A; 245 C; 231 G; 401 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 2,92e-112 Length: 1173  
 Score: 1370.50 Matches: 267  
 Percent Similarity: 78.32% Conservative: 40  
 Best Local Similarity: 68.11% Mismatches: 82  
 Query Match: 66.92% Indels: 3  
 DB: 6 Gaps: 2  
 US-10-626-445-8 (1-391) x AA167750 (1-1173)  
 QY 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaIleValIleProLeuAlaPhe 20  
 DB 1 ATGCCAATACCTAATACCAATCAATTAATCACTAAGCACTCGTGAATCTTAAGCAATT 60  
 QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40  
 DB 61 TTTATGCTCTTAAGTACTTTTGGCTAATAATGCTAGAAATGTTGGTCATTTAAGCTTTT 120  
 QY 41 ValValAspArgAsnLeuAArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 DB 121 GTGGTGGACAAACCTTAGCATCGAAGTAGTATATTTTCTTAATCTGGCCATCTCT 180  
 QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80  
 DB 181 GACTCTCTTTGGGTGGTGAATCTCCATTCCTTGTACATCCCTCAACAGCGTGTGAAATGG 240  
 QY 81 AsnPheGlySerGlyIleCysMetPheTyrPheLeuIleThrAspTyrLeuLeuCysThrAla 100  
 DB 241 GATTTTGGAAAGAAATCTGTGATTTTGGCTACTGACTGATCTGTATATGACAGCA 300  
 QY 101 SerValTyrAsnIleValIleLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 301 TCTGTATATAAATTCCTCATCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 360

QY 121 SerTyrArgAlaGlnHisThrGlyIleMetLeuIleValAlaGlnMetValAlaValTyr 140  
 DB 361 AGTTATAGAACTCAACATACCTAGGCTCTTGAAGATTTTACTGTGATGATGATGATGATGATGAT 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrPheAsnSer 160  
 DB 421 GTCTGGCTCTTCTTAGTAAGTAAGGCGCAATGATTTCTAGTTTCAAGATCTTGAAGGATGAA 480  
 QY 161 ThrAsnThrTyrAspCysGluProGlyPheValIleThrGluTyrTyrIleLeuThrIleThr 180  
 DB 481 GGTAAGT-----GAATGTGAACCTGGATTTTCTGGAAATGGTACATCTTGGCATCACA 534  
 QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
 DB 535 TCATCTTGGAATTCGGATCCAGTATCTTGTAGTGGCTTATTTCAACATGATATTTAT 594  
 QY 201 TyrSerLeuTyrPheArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
 DB 595 TGGAGCTGTGGAAGCGTATCATCTCAGTAGGTCGCAAGCCATCCGTGACTGACTGCT 654  
 QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
 DB 655 GTCTCTTCCAAATCTGTGACACTCATTCAGAGTAGACTATCTTCAGAGAGATCTT 714  
 QY 241 ProGlyLeuLeuGluSerAlaAlaSerArgHisSerGluSerProArgArgTyrSerSer 260  
 DB 715 TCTGCATCCAGCAAGAACTCTGATCTTCTTCACTAGAGAGAGAGAGAGAGAGAGT 774  
 QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheValGlySer 280  
 DB 775 CTGATGTTTCTTCAAGAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 834  
 QY 281 PheTyrArgSerLeuSerAlaAlaLeuArgGlnArgGlyTyrAlaGluLeuLeuArgGly 300  
 DB 835 TTTCTCCCAATCAATTTCTGAGCTTTCACCAAAAGGAGACATGTAATGCTCAGAGCC 864  
 QY 301 ArgLeuLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrPalaPro 320  
 DB 895 AGGAGATTAGCCAAAGTACATCGGCCATTTCTTGAAGGTTTCTGTTGCTGGGCTCCA 954  
 QY 321 TyrCysLeuPheThrIleValIleLeuSerThrTyrProArgThrGluArgProLysSerVal 340  
 DB 955 TATTTCTGTGTCAAAATTTGCTTTCATTTATTTCTTCACCAACAGGCTCTTAATCATGTT 1014  
 QY 341 TyrPyrSerIleAlaPheTyrPheLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360  
 DB 1015 TGGTATAGAAATTCATTTTGGCTTCAGTGGTTCAAATTCCTTTCATTCCTCTTTGTAT 1074  
 QY 361 ProLeuCysHisArgArgPheGlnIleValAlaPheTyrPheIleLeuCysValIleThrLysTyr 380  
 DB 1075 CCAATTTGTCAACAAGCCTTTCAAAAAGCCTTTCTTGAAATATTTTGTATATAAAAAGCAA 1134  
 QY 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391  
 DB 1135 CTTCTACATCAACAACACAGTCGTCAGTATCTTCT 1170  
 RESULT 13  
 ACA93262  
 ID ACA93262 standard; cDNA; 1173 BP.  
 AC ACA93262;  
 XX 16-JUL-2003 (first entry)  
 DE Human cDNA encoding GPCR hRUP7.  
 XX Human; se; gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;  
 KW hARE-5; hRUP5; hRUP6; hRUP7; hGPCR27; hARE-1; hARE-2; hPR1; hG2A;  
 KW hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hRUP4; signaling cascade.  
 XX Homo sapiens.  
 OS



FN US2003017528-A1.  
 XX  
 PD 23-JAN-2003.  
 XX  
 PF 06-JUN-2001; 2001US-00875076.  
 XX  
 PR 20-NOV-1998; 98US-0109213P.  
 PR 16-FEB-1999; 99US-0120416P.  
 PR 26-FEB-1999; 99US-0121852P.  
 PR 12-MAR-1999; 99US-0123946P.  
 PR 12-MAR-1999; 99US-0123949P.  
 PR 28-MAY-1999; 99US-0136436P.  
 PR 28-MAY-1999; 99US-0136437P.  
 PR 28-MAY-1999; 99US-0136439P.  
 PR 28-MAY-1999; 99US-0136567P.  
 PR 28-MAY-1999; 99US-0137127P.  
 PR 28-MAY-1999; 99US-0137131P.  
 PR 29-JUN-1999; 99US-0141448P.  
 PR 28-SEP-1999; 99US-0156333P.  
 PR 29-SEP-1999; 99US-0156555P.  
 PR 29-SEP-1999; 99US-0156634P.  
 PR 12-OCT-1999; 99US-00417044.  
 XX  
 PA (CHEN/) CHEN R.  
 PA (DANG/) DANG H T.  
 PA (LIAM/) LIAM C W.  
 PA (LINI/) LIN I.  
 XX  
 PI Chen R, Dang HT, Liam CW, Lin I;  
 DR WPI; 2003-428952/40.  
 DR P-PEDB; ABU92265.  
 XX  
 PT Novel endogenous, orphan, human G protein-coupled receptors useful for  
 PT identification of modulators of the receptor and as research tools for  
 PT understanding the role of the receptor in human body.  
 XX  
 PS Claim 25; Page 22; 54pp; English.  
 CC The invention relates to a human G protein-coupled receptor (GPCR)  
 CC appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named  
 CC hARE-3, hARE-4, hARE-5, hRUP3, hRUP5, hRUP6, hRUP7, hGCR27, hARE-1, hARE  
 CC -2, hPRP1, hGNA, hCHN4, hCHN6, hCHN8, hCHN9, hCHN10 and hRUP4.  
 CC Also included are a plasmid comprising a vector and one of the cDNAs  
 CC above and a host cell comprising the plasmid. The GPCRs are useful for  
 CC the direct identification of candidate compounds as inverse agonists,  
 CC agonists or partial agonists. In vitro and in vivo systems incorporating  
 CC GPCRs is useful for elucidating and understanding the roles these  
 CC receptors play in the human condition, both normal and diseased, as well  
 CC as understanding the role of constitutive activation as it applies to  
 CC understanding the signalling cascade. The cDNAs are useful for making a  
 CC probe for dot-blot analysis against tissue mRNA and/or RT-PCR  
 CC identification of the expression of the receptor in tissue samples. The  
 CC present sequence is a cDNA encoding a GPCR of the invention  
 XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2,92e-112 Length: 1173  
 Score: 1370.50 Matches: 267  
 Percent Similarity: 78.32% Conservative: 40  
 Best Local Similarity: 68.11% Mismatches: 82  
 Query Match: 66.92% Indels: 3  
 DB: 8 Gaps: 2  
 US-10-626-445-8 (1-391) x ACA93262 (1-1173)  
 QY 1 MetSerGluSerAsnSerThrGlyIleuProPheAlaGlnValProleuAlaPhe 20  
 DB 1 ATGCCAGATCAATGACCAATCAATTTATCACTAAGACCTGGTATACCTTACATT 60  
 QY 21 LeuMetSerSerPheAlaPheAlaIleuMetValGlyAsnAlaValValIleuAlaPhe 40

DB 61 TTTATGCTCTTAGAGCTTTTGGCTATTAATGCTAGAAATGCTTGGTCACTTTAGCTTTT 120  
 QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 DB 121 GTGGTGACAAAACCTTAGACATGACATGATATTTTCTTTTCTTAACTGGCCATCTCT 180  
 QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80  
 DB 181 GACTCTCTTGTGGGTGATGATCTTCATTTCTTTGTATGATCCCTCACACGCTGTTCCGATGG 240  
 QY 81 AsnPheGlySerGlyIleCysMetCysPheTyrPheValIleThrAspTyrLeuLeuGlySerHisAla 100  
 DB 241 GATTTTGGAAAGAAATCTGTATTTTGGCTTGGCCACTGACTGATCTGTATGATGACAGA 300  
 QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 301 TCTGTATATACATTTGCTCTTCACGCTATGATGACATCTGCTGATCTTCAAAAGCTGTG 360  
 QY 121 SerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTyr 140  
 DB 361 TCTTATAGAACCAACATACCTGGGCTCTTGAAGATTTGTTACTGTATGGTGGCCGTTTGG 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrPheAsnSer 160  
 DB 421 GTGCTGGCCTTCTTATGTAATGGCCAAATGATTTCTAGATTCAGACTCTTGAAGGATGAA 480  
 QY 161 ThrAsnThrTyrAspCysGluProGlyPheValIleThrGluTyrTyrIleuThrIleThr 180  
 DB 481 GGTAGT-----GAATGTGAACCTGATTTTGTGGAAATGATATCTTCCATCACA 534  
 QY 181 MetLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
 DB 535 TCATCTTGGAATTCGTATCCCACTCATCTTAGTCGCTTATTTCAACATGATATTTAT 594  
 QY 201 TyrSerIleTyrPheArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
 DB 595 TGGACCTGTGGAAAGCTGATCATCTCAGTAGGTCCAAAGCCATCTGGAATCTGCTGCT 654  
 QY 221 ThrSerSerSerAlaSerGlyHisIleuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
 DB 655 GTCTTTCACATCTGTGGACACCTCATTCAGAGGTAGCATATCTTCAAGGAGATCTCTT 714  
 QY 241 ProGlyLeuValGluSerAlaIleSerArgHisSerGluSerProArgArgHisSerSer 260  
 DB 715 TCTGATGACACAGAACTTCCGATCTCTTCACTTATGAGACACACAGAGAAAGATGAT 774  
 QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheValValGlySer 280  
 DB 775 CTCATGTTTCTCTCAAGAACCAAGATGATGATCAATGATTCATCCAAATGGGTTCC 834  
 QY 281 PheTyrArgSerGluSerAlaIleuArgGlnArgTyrValGluLeuLeuArgGly 300  
 DB 835 TTTCTCCCATCATGATCTGTGCTCTTCAACAAAGGAAACATGTGAATCTGTTAGAGCC 894  
 QY 301 ArgValAlaIleArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysThrAlaPro 320  
 DB 895 AGGAGATTAGCCAACTGCTGCAATCTCTTAGGGGTTTGTGCTGTTGCTGGGCTCCA 954  
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLeuSerVal 340  
 DB 955 TATTCTCTGTTCAACAATTTGCTCTTTATTTATTCCTCAGCAACAGGCTTAATACAGTT 1014  
 QY 341 TrpTyrSerIleAlaPheTyrPheGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360  
 DB 1015 TGGTATGAATTTGCTTTGGCTTCAGTGTTCATATCTTTGTCAATCTCTTTTGTAT 1074  
 QY 361 ProLeuCysHisArgArgPheGlnIleValAlaPheTyrPheValIleLeuCysValThrTyrTrp 380  
 DB 1075 CCAATTGTGCACAAAGCCTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAGCA 1134  
 QY 381 ProAlaLeuSerGln--AsnGlnSerValSerSer 391  
 DB 1135 CCTTACATCAACAACAGTGGCTGATATCTTCT 1170

RESULT 14  
ADG98759  
ADG98759 standard; cDNA; 1173 BP.  
AC ADG98759;  
XX  
XX 11-MAR-2004 (first entry)  
XX DE Human orphan GPCR cDNA, RUP7.  
XX Human; G protein-coupled receptor; GPCR; research tool; gene; ss.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1173  
FT /\*tag= a  
FT /product= "Human GPCR protein"  
PN US2003148450-A1.  
XX  
XX 07-AUG-2003.  
XX  
XX 17-OCT-2002; 2002US-00272983.  
XX  
XX 20-NOV-1998; 98US-0109213P.  
XX 16-FEB-1999; 99US-0120416P.  
XX 26-FEB-1999; 99US-0121852P.  
XX 12-MAR-1999; 99US-0123946P.  
XX 12-MAR-1999; 99US-0123949P.  
XX 28-MAY-1999; 99US-0136436P.  
XX 28-MAY-1999; 99US-0136437P.  
XX 28-MAY-1999; 99US-0136439P.  
XX 28-MAY-1999; 99US-0136567P.  
XX 28-MAY-1999; 99US-0137127P.  
XX 28-MAY-1999; 99US-0137131P.  
XX 29-JUN-1999; 99US-0141448P.  
XX 28-SEP-1999; 99US-0156333P.  
XX 29-SEP-1999; 99US-0156555P.  
XX 29-SEP-1999; 99US-0156549P.  
XX 12-OCT-1999; 99US-00417044.  
XX  
XX (CHEN/) CHEN R.  
XX (DANG/) DANG H T.  
XX (LIAN/) LIAN C W.  
XX (LIN/) LIN I.  
XX  
XX Chen R, Dang HT, Lian CW, Lin I;  
XX  
XX WPI: 2003-897571/82.  
XX P-PSDB; ADG98760.  
XX  
XX New cDNA encoding a human G protein coupled receptor, useful for making a  
XX PT probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR  
XX PT identification of the expression of the receptor in tissue samples.  
XX  
XX Claim 25; SEQ ID NO 13; 52bp; English.  
XX  
XX The present invention provides novel human G protein-coupled receptor  
XX (GPCR) proteins and their encoding nucleic acids. The invention is useful  
XX for making a probe for dot-blot analysis and for RT-PCR identification of  
XX the expression of the receptor in tissue samples. The invention is also  
XX useful for identifying candidate compounds as inverse agonists, agonists  
XX or partial agonists and as research tools in determining the location of  
XX the receptors within the body. The present sequence is human orphan G  
XX protein-coupled receptor cDNA.  
XX  
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
Alignment Scores: 2.92e-112 Length: 1173  
Pred. No.: 1370.50 Matches: 267  
Score:

Percent Similarity: 78.32%  
Best Local Similarity: 68.11%  
Query Match: 66.92%  
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Gaps: 2  
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QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40  
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QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuLeuAlaIleSer 60  
DB 121 GTGGTGACAAATAACCTTAGACATCGAAGTAGTATTTTCTTTAATCTGGCATCTT 180  
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80  
DB 181 GACTTCTTTGGGGTGATCTCATTCCTTTGTAATCCCTCACACGCTGTCGAATGG 240  
QY 81 AsnPheGlySerGlyIleCysMetPheTyrPheIleThrAspTyrIleLeuLeuCysThrAla 100  
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QY 101 SerValTyrAsnIleValIleIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
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QY 121 SerTyrArgAlaGlnHisThrGlyIleMetLeuIleValAlaGlnMetValAlaValTyr 140  
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QY 161 ThrAsnThrIleValAspCysGlyProGlyIlePheValThrGlyIleTyrIleLeuThrIleThr 180  
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DB 535 TCATCTTGGAATTCGATGCCATCCATCATCTTGTGCTTATTCACATGAATATTAT 594  
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QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
DB 655 GTCTCTTCCAAACTCTGTGACACTCATTCAGAGTAGACTATCTTCAGAAAGATCTCTT 714  
QY 241 ProGlyLeuIleGlnSerAlaIleSerArgHisSerGlnSerProArgArgIleSerSer 260  
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QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheIleValGlySer 280  
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DB 895 AGAGATTAACCAAGTACATCGGCATCTTCTTAGGGGTTTCTGCTTCTGCGCTCCA 954  
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGlnArgProIleValSerVal 340

DB 955 TATCTCTGTTCAACATTCCTTCATTATTTCTCTCAGCAACAGTCTCAATCATGTT 1014  
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QY 361 ProLeuCySHisArgArgPheGlnIleValAlaPheTrpIleLeuCyValThrIleTrp 380  
DB 1075 CCATTGTGTCAACACCGCTTCAAAAGCTTCTTGAAAATTTTGTATATAAAGCAA 1134  
QY 381 ProAlaLeuSerGln--AasnIleSerValSerSer 391  
DB 1135 CCTTACCATCACAACACAGTGGTCAATCTTCT 1170  
RESULT 15  
AB557063 standard; cDNA, 1173 BP.  
AC AB557063;  
XX 28-JAN-2003 (first entry)  
DT Human cDNA encoding G-protein coupled receptor AXOR35.  
XX Human; ss; gene; G-protein coupled receptor; AXOR35; lymphocyte;  
KW macrophage; eosinophil; neutrophil; infection; transplant rejection;  
KW gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;  
KW Crohn's disease; irritable bowel syndrome; vomiting; inflammation;  
KW atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;  
KW psoriasis; urological disease; urinary retention; cardiovascular disease;  
KW myocardial infarction; hypertension; hypertension; pulmonary disorder;  
KW chronic obstructive pulmonary disease; cough; renal disease;  
KW renal ischaemia; arteriosclerosis; atherosclerosis; psychosis;  
KW neurological disorder; migraine; anorexia; anxiety; schizophrenia;  
KW dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;  
KW graft versus host disease; osteoporosis.  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FT CDS 1..1173  
FT /\*tag= a  
FT /product= "AXOR35"  
XX US200237054-A1.  
XX 26-SEP-2002.  
XX 20-JUL-2001, 2001US-00910411.  
XX 02-NOV-1999; 99US-00431898.  
XX 03-FEB-2000; 2000US-00497790.  
XX 20-OCT-2000; 2000US-00693761.  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
XX Aubart KM, Bergema DJ, Fitzgerald L, Graybill TL, Li X,  
XX Michalovich D, Morrow DM, Zhu Y,  
XX WPI; 2003-074982/07.  
XX P-PSDB; ABG71960.  
XX Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for  
XX treating infections, gastrointestinal disorders, autoimmune disorders,  
XX urological diseases, cardiovascular diseases and cancer.  
XX Claim 2; Page 21-22; 24pp; English.  
XX The invention relates to an isolated G-protein coupled receptor  
XX polypeptide, AXOR35, (and its homologues and variants) and its encoding  
XX polynucleotide (and its homologues, variants, complements and RNA  
XX equivalents). Also included are an anti-AXOR35 antibody, an AXOR35

CC expression vector, producing a recombinant host cell by introducing the  
CC vector into a cell such that the host cell produces AXOR35, a membrane of  
CC the host cell expressing AXOR35, identifying/screening for agonists or  
CC antagonists of AXOR35 and inhibiting or promoting the function of  
CC lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,  
CC by administering to the patient AXOR35 agonists or antagonists. The  
CC agonist or antagonist identified is useful for treating a disease such as  
CC asthma, or for inhibiting or promoting the function of lymphocytes,  
CC macrophages, eosinophils, or neutrophils in diseased tissue such as an  
CC asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays,  
CC for identifying compounds that are agonists or antagonists of AXOR35, as  
CC vaccines, or for treating infections (bacterial, fungal, protozoan or  
CC viral infections), transplant rejection, gastrointestinal disorders (such  
CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),  
CC irritable bowel syndrome, vomiting, inflammation (such as atopic  
CC dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,  
CC psoriasis), urological diseases (such as urinary retention),  
CC cardiovascular diseases (such as myocardial infarction), hypertension,  
CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary  
CC disease), cough, renal diseases (such as renal ischaemia),  
CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders  
CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such  
CC as Parkinson's disease), cancer, obesity, stroke, septic shock, graft  
CC versus host disease and osteoporosis. The present sequence is the cDNA  
CC encoding AXOR35  
SQ Sequence 1173 BP, 294 A, 245 C, 231 G, 403 T, 0 U, 0 Other;  
Alignment Scores:  
Pred. No.: 2,92e-112 Length: 1173  
Score: 1370.50 Matches: 267  
Percent Similarity: 78.32% Conserved: 40  
Best Local Similarity: 68.11% Mismatches: 82  
Query Match: 66.92% Gaps: 3  
DB: 10 Gaps: 2  
US-10-626-445-8 (1-391) x AB557063 (1-1173)  
QY 1 MetSerGluSerAsnSerThrGlyIleuProPheAlaGlnValProLeuAlaPhe 20  
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QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTrpPhePheAsnLeuAlaIleSer 60  
DB 121 GTGGTGACAAATAACCTTAGACATGAGTAGTATTTTCTTAACTTGGCCATCTCT 180  
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTrpIleProHsValLeuPheAsnTrp 80  
DB 181 GACTCTCTTGGGGTGATCTCCATTCCTTTGTACATCCCTCACACCGCTTGGAAATGG 240  
QY 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTrpLeuLeuCyThrAla 100  
DB 241 GATTTTGGAAAGAAATCTGTGATTTTGGCTCACTAGTACGTATCTGTATAGACACA 300  
QY 101 SerValTyraenIleValLeuIleSerTyraPargTrpGlnSerValSerAsnAlaVal 120  
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QY 121 SerTyraArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTrp 140  
DB 361 TCTTATGAACTCAACATCACTAGGCTCTTGAAGATTTGTACTTGATGATGCGCTTTGG 420  
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160  
DB 421 GTGCTGGCTCTTCTTAAGTAAAGGCAATGATTTCTAGTCTTGAAGAGATCAA 480  
QY 161 ThrSerThrIleAspCysGluProGlyPheValThrGluTrpTrpIleLeuThrIleThr 180  
DB 481 GGTAGT-----GATGTGAACCTGGATTTTTCGGAATGTATCTCTTGCATCA 534

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Db 535 TCATTCTTGGAATTCGGATCCCAAGTCATCTTAGTCCTTATTTCACATGAAATATTAT 594
Qy 201 TTPSerLeuTTPlySArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 595 TGGAGCCTGTGGAAGCCTGATCATCTCAGTAGGTGCCAAAGCCATCTCGGACTGACTGCT 654
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCTCTTCCAACTCTGTGACACTCATTCAGAGTAGACTATCTTCAGAGAGATCTCTT 714
Qy 241 ProGlyLeuLySArgAlaAlaSerArgHisSerGlySerProArgArgLySArgSer 260
Db 715 TCTGCATCCGACAGAGATTCCTGCATCTTTCATTCAGAGACAGAGAGAAAGAGTAGT 774
Qy 261 HisLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLySValGlySer 280
Db 775 CTCATGTTTTCCTCAAGAACCAAGATGAAATAGCAATATGCTTCCAAATGGGTTCC 834
Qy 281 PheThrArgSerGlySerAlaAlaLeuArgGlnArgGluTyrAlaGlyLeuLeuArgGly 300
Db 835 TTCTCCCAATCAAGATTCGTAGCTCTTCACCAAGGGAACAATGTTGAACTGCTTAGACC 894
Qy 301 ArgLySLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGCTGTGCTGGGCTCCA 954
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Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1015 TGGTAATAGAAATGCAATTTGGCTTCAGTGTCAATTCCTTGTCAATCCTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLySAlaPheTrpLySLeuLeuCysValThrLySTrp 380
Db 1075 CCATTGTGTCAACAAGCCTTTCAAAAGCCTTCTTGAAAATATTTTGTATATAAAAGCAA 1134
Qy 381 ProAlaLeuSerGln--AasnInSerValSerSer 391
Db 1135 CCTTACCATCACAAACAGTGGGTGATCTTCT 1170
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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	724.5	35.4	2665	4	US-09-949-016-5059
4	724.5	35.4	2689	2	US-08-985-090-1
5	724.5	35.4	2689	3	US-09-165-543-1
6	724.5	35.4	2699	3	US-09-167-354-5
7	724.5	35.4	2699	3	US-09-642-855-5
8	724.5	35.4	2699	3	US-09-642-855-5
9	722.5	35.3	1335	2	US-08-985-090-3
10	722.5	35.3	1335	3	US-09-165-543-3
11	722.5	35.3	1335	3	US-09-167-354-6
12	722.5	35.3	1335	3	US-09-642-855-6

13	722.5	35.3	1335	3	US-09-642-514-6	Sequence 6, Appl1
14	722.5	35.3	2050	4	US-09-891-053-21	Sequence 21, Appl1
15	716.5	35.0	1338	3	US-09-165-543-6	Sequence 26, Appl1
16	716.5	35.0	1953	4	US-09-891-053-26	Sequence 2, Appl1
17	716.5	35.0	3244	3	US-09-165-543-4	Sequence 4, Appl1
18	709.5	34.6	1239	4	US-09-891-053-2	Sequence 5, Appl1
19	709.5	34.6	2700	4	US-09-891-053-5	Sequence 6, Appl1
20	624.5	30.5	1056	3	US-09-524-162-1	Sequence 3, Appl1
21	582.5	28.4	1086	2	US-08-985-090-6	Sequence 33, Appl1
22	582.5	28.4	1086	2	US-09-165-543-33	Sequence 4, Appl1
23	582.5	28.4	2218	2	US-08-985-090-4	Sequence 31, Appl1
24	582.5	28.4	2218	3	US-09-165-543-31	Sequence 6, Appl1
25	415.5	20.3	1956	1	US-08-313-553-6	Sequence 13, Appl1
26	415.5	20.3	1956	3	US-08-767-993-6	Sequence 13, Appl1
27	413	20.2	1422	4	US-09-016-434-1339	Sequence 520, App
28	408	19.9	1422	4	US-09-826-509-512	Sequence 516, App
29	404.5	19.8	1913	4	US-09-016-434-1314	Sequence 8, Appl1
30	404.5	19.8	2261	4	US-09-016-434-1176	Sequence 1176, Ap
31	401	19.6	1893	4	US-09-891-053-13	Sequence 13, Appl1
32	401	19.6	9293	4	US-09-949-016-16801	Sequence 16801, A
33	399.5	19.5	1599	4	US-09-826-509-520	Sequence 516, App
34	399.5	19.5	1773	4	US-09-826-509-516	Sequence 516, App
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42	390	19.0	2140	1	US-08-468-939-1	Sequence 1, Appl1
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44	390	19.0	2140	2	US-08-722-190-1	Sequence 1, Appl1
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#### ALIGNMENTS

RESULT 1  
US-09-414-010-1  
Sequence 1, Application US/09414010  
Patent No. 6204017  
GENERAL INFORMATION:  
APPLICANT: Behan, Jiang Xu  
APPLICANT: Hedrick, Joseph A.  
APPLICANT: Kaz, Thomas M.  
APPLICANT: Monema, Frederick J. Jr.  
APPLICANT: Morse, Kelley L.  
APPLICANT: Umland, Shelby P.  
APPLICANT: Wang, Suke  
TITLE OF INVENTION: Histamine receptor  
FILE REFERENCE: CNO1069  
CURRENT APPLICATION NUMBER: US/09/414,010  
CURRENT FILING DATE: 1999-10-07  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1173  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-414-010-1

Alignment Scores:  
Pred. No.: 5.02e-133  
Score: 1370.50  
Percent Similarity: 78.32%  
Best Local Similarity: 68.11%  
Query Match: 66.92%  
DB: 3  
Gaps: 2

US-10-626-445-8 (1-391) x US-09-414-010-1 (1-1173)  
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Ds	301	TCTGTATATATACATTTGCTCTCAACAGCTATGATGATACATCTGTCAAGTCCAAATCTGTG	360
Oy	121	SerTYrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTrp	140
Ds	361	TCTTATATAGACCTCAACATATCGGGGCTTGAAGATTTGTTACTGTATGCTGGCCGTTTGG	420
Oy	141	IleIleuAlaPheIleuValAsnGlyProMetIleIleuAlaSerAspSerTrpIlyAsnSer	160
Ds	421	GTGCTGGCCCTTCTTATGTGATGGGCCAAATGATTTCTTATTCAGAGCTTGGAAAGATGAA	480
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Ds	481	GGTACT-----GAATGTGAACTGTGATTTTGGAAATGGTAACTCTTGCCATCACAA	534
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Oy	201	TrpSerIleuTrpIlyArgAlaIleuSerArgCYsProSerHisAlaGlyPheSerThr	220
Ds	595	TGGAACCTGTGGAAACGTATCATCTCAATGATGTGGCAAAAGCATCTGTGACTGCT	654
Oy	221	ThrSerSerSerAlaSerGlyHisIleuHisArgAlaGlyValAlaCYArgThrSerIen	240
Ds	655	GTCTCTTCCAAATCTGTGGACACATTCACAAAGGTAGTACTTCTTCAAGAGATCTCTT	714
Oy	241	ProGlyLeuIlyGlnSerAlaIleSerArgHisSerGlnSerProArgArgIlySerSer	260
Ds	715	TCTGCATGACAGAAAGTCTCTGCATCTCTTCACTTACAGACAGACAGAAAGATGACT	774
Oy	261	IleIleuValSerIleuArgThrHisMetAsnSerSerIleHisAlaPheIlyValGlySer	280
Ds	775	CTCAATGTTTTCTTCAAGAACCAAGATGAAATAGCATACAAATGCTTCCAAATGGGTTCC	834
Oy	281	PheTrpArgSerGlnSerAlaIleuAlaIleuArgGlnGlyTYrAlaGlnIleuIleuArgGly	300
Ds	835	TTCTCCCAATCAGATTCGTACTCTTTCACAAAGGAAACATGTTGAACTGCTTGAAGCC	894
Oy	301	ArgIlySerAlaArgSerIleuAlaIleIleuLeuSerAlaPheAlaIleCYsrTrpAlaPro	320
Ds	895	AGGAATATAGCAAGTCACTGGCCATTTCTTTAAGGGGTTTTTGTCTGTGGCTGGGCTCA	954
Oy	321	TYrCYsLeuPheThrIleValIleuSerThrTYrProArgThrGlnArgProIlySerVal	340
Ds	955	TATTCCTGTTCCACAAATGCTCTTCAATTATTCCTCAGCAACAGGTCCTAAATCAGATT	1014
Oy	341	TrpTYrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTYr	360
Ds	1015	TGGTATATACATTTGCAATTTGGCTTCAAGTGTTCAATTTCTTGTGCAATCTCTTTTGTAT	1074
Oy	361	ProIleuCYHisArgArgPheGlnIlyAlaPheTrpIlyIleIleuCYValHisIlySerTrp	380
Ds	1075	CCATTTGTGTCACAAAGGCTTTCAAAAGGCTTTCTTGAAATAATTTGTATATAAAGCA	1134

```

QY      381 ProAlaLeuSerGln--AasnIndserValSerSer 391
          |||         |||||         ::::~::~|||
Db      1135 CCTTACCAATCACAACAGCGTGCTGCATGATTCCT 1170

RESULT 2
US-09-812-216-1
; Sequence 1, Application us/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, JIang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CNO1069
; CURRENT APPLICATION NUMBER: US/09/812,216
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1

Alignment Scores:
Pred. No.:           5,02e-133             Length:           1173
Score:              1370.50                 Matches:            267
Percent Similarity: 78.32%                  Conservative:       40
Best Local Similarity: 68.11%                Mismatches:        82
Query Match:        66.92%                   Indels:             3
DB:                 4                       Gaps:               2

US-10-626-445-8 (1-391) x US-09-812-216-1 (1-1173)

QY      1 MetSerGlnSerAsnSerThrcGlyIleuProProAlaAlaGlnValProLeuAlaPhe 20
          ::::::::::::::::::::|||         ::: ~::|||
Db      1 ATGCCAGATTACTAAATAGCACCATCATTTATCATCTACTACACACCTCGTGTACTTAGCATTTT 60

QY      21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleuAlaPhe 40
          |||||         |||||         |||||         |||||         |||||         |||||
Db      61 TTATAGTCCTTAGTAGCTTTTCCTTAATGCTAGGAATAAGCTTGGTCATTTTAGCTTTT 120

QY      41 ValValaAParGAsnLeuAlaGHisArgSerAsnTyrrPhePheLeuAsnLeuAlaIleSer 60
          ::::::::::::::::::::|||         ::: ~::|||
Db      121 GTGGTGGAACAATAACCTTAGACATCGAAGTAGTATTTTTTTCTTAACCTTGGCCAATCTCT 180

QY      61 AsnPheLeuValGlyLeuIleSerIleProLeuTyrrIleProHisValLeuPheAsnTrp 80
          ::::::::::::::::::::|||         ::: ~::|||
Db      181 GACTTCTTTGGGGGTGATGTCCTCATTTCTTTGTACATCCCACACCGCTGTTCGAATGG 240

QY      81 AsnPhcGlySerGlyIleCysewecPheTrpLeuIleThrAspTyrrLeuDeuCysTrpAla 100
          ::::::::::::::::::::|||         ::: ~::|||
Db      241 CATTTTGAAGAAGAAATCTGTGTATTTTGGCTCACTACGATTAATCTGTTATGTACAGA 300

QY      101 SerValTyrrAsnIleValLeuIleSerTyrrAspArgTyrrGlnSerValSerAsnAlaVal 120
          ::::::::::::::::::::|||         ::: ~::|||
Db      301 TCTGTATTAATCAATGCTCCTCATCACTATGATCATACCTGTCAAGTCTCAATAGCTGTG 360

QY      121 SerTyrrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140
          ::::::::::::::::::::|||         ::: ~::|||
Db      361 TCTTATTAACAACCTCAACATCTGGGGGTCTTGAAGATTTGTTACTGTATGTGTGGCCGTTTGG 420

QY      141 IleIeuAlaPheLeuValAsnGlyProMetIleIeuAlaSerAspSerTrpLysAsnSer 160
          ::::::::::::::::::::|||         ::: ~::|||
Db      421 GTGCTGGCTTCTTAGTGAATGGCCCAATGATTTCTTAGTTTCAAGAGCTTGGAAAGGATGAA 480

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QY 161 ThrAenThrlyeAspCygluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
   ::::::::::::::::::::
Db 481 GGTAGT-----GATGTGAACCTGGATTTTTCGGATGTGACTCTTCCATCA 534
QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValIleTyrPheAsnValGlnIleTyr 200
   ::::::::::::::::::::
Db 535 TCATCTTGGATTCGTGATCCAGTCATCTTAGTCGTTATTTCAACATGATATTAT 594
QY 201 TRPSeuLeuTrpLysArgIleValLeuSerArgCysProSerHisIleValIlePheSerThr 220
   ::::::::::::::::::::
Db 595 TGGACCCGTGGAGAGGTATCATCTCAGTAAAGTCCAAAGCCATCTCGACTGACTGCT 654
QY 221 ThrSerSerSerAlaSerGlyHisIleuHisArgAlaGlyValAlaCysArgThrSerAsn 240
   ::::::::::::::::::::
Db 655 GTCTCTTCCAACTGTGGACATCATTCACAGAGAGAGATCTTCAAGAGATCTTCT 714
QY 241 ProGlyLeuLysGluSerAlaIleSerArgHisSerGluSerProArgIleLysSerSer 260
   ::::::::::::::::::::
Db 715 TCTGCATCGACAGAAAGTTCCTGATCTCTTTCATTCAGAGACAGAGAGAGAAAGTAGT 774
QY 261 IleLeuValSerLeuArgThrHisMetLeuSerSerIleThrAlaPheLysValGlySer 280
   ::::::::::::::::::::
Db 775 CTGATGTTTCTCAGAAACCAAGATGATAGCAATACCAATTGCTCCAAATGGGTTCC 834
QY 281 PheTrpArgSerGluSerAlaIleValArgIleValArgIleValArgIleValArgIle 300
   ::::::::::::::::::::
Db 835 TTCTCCCAATCAGATTCGTAGCTCTTCCACCAAGGAGACATGTTGAATCTTGAAGCC 894
QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
   ::::::::::::::::::::
Db 895 AGGAGATTAGCCAGACGACTGGCCATCTTAGGGGTTTTCGCTGTTGCTGGGCTCA 954
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
   ::::::::::::::::::::
Db 955 TATTCCTGTTCCACATGTCTTTCATTTTCTCTCAGCAACAGGCTCTTAATCAGTT 1014
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
   ::::::::::::::::::::
Db 1015 TGGTATGAAATTCATTTGGCTTCAGTGGTTCATTTCTTGTCAATCTCTTTGTTAT 1074
QY 361 ProLeuCyHisArgArgPheGlnLysValaPheTrpLysIleLeuCyHisValThrLysTrp 380
   ::::::::::::::::::::
Db 1075 CCATTGTGTCAACAGCGCTTCAAAAGGCTTCTTGAAAATATTTGTATATAAAGCA 1134
QY 381 ProAlaLeuSerGln--AsnGlnSerValSerSer 391
   ::::::::::::::::::::
Db 1135 CCTTACCATCACAACACAGTCGTCAATCTTCT 1170

RESULT 3
US-09-949-016-5059
; Sequence 5059, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5059
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5059
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Alignment Scores:
Pred. No.: 4,8e-65 Length: 2665
Score: 724.50 Matches: 171
Percent Similarity: 48.90% Conservative: 52
Best Local Similarity: 37.50% Mismatches: 118
Query Match: 35.38% Indels: 115
DB: 4 Gaps: 12

US-10-626-445-8 (1-391) x US-09-949-016-5059 (1-2665)
QY 18 LeuAlaPheLeuMetSerSerPheAlaPheValIleMetValGlyAsnAlaValIle 37
   ::::::::::::::::::::
Db 400 CTGGCCGCGCTCATGGCTGCTCATCGTGCACAGCGTGGGCAAGCGCGTGCATCG 459
QY 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerArgThrPhePheLeuAsnLeu 57
   ::::::::::::::::::::
Db 460 CTCGCTTCGTGGCCGAGCTCGAGCTCGCAACCCAGAACACTTCTTCCTGCAACCTC 519
QY 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
   ::::::::::::::::::::
Db 520 GCCATCTCGACTTCTCTGTCGCGCCCTTTCGATCCCATCTGATACCTTAAGTCTGCTG 579
QY 78 Phe--AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
   ::::::::::::::::::::
Db 580 ACAGCGCCGCTGACCTTGGCGCGGCGCTCGCAAGCTGTGGCTGTAGTGAATACCTG 639
QY 97 LeuCyThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
   ::::::::::::::::::::
Db 640 CTGTGCACCTCTCTGCTCAACATCGTGCATCACTACAGACCTGCTTCCTGCTGGCTG 699
QY 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
   ::::::::::::::::::::
Db 700 ACCCGAGCGGTCTCATACCGGCGCCAGCGGTACACGCGGCGCGAGCTGGCAAGATG 759
QY 137 ValAlaValIleTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
   ::::::::::::::::::::
Db 760 CTGCTGCTGTGGGTCTGCTGCTCTCTGCTGTAAGCAGCAGCATCTG-----AGC 810
QY 157 TrpLys-----AsnSerThrAsnThrLysAspCygluProGlyPheVal 171
   ::::::::::::::::::::
Db 811 TGGGAGTACTGTCCGCGGGGAGCTCCATCCCGAGGCGCACTGTATGCCAGTTCTTC 870
QY 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuGluPheLeuProValIleSer 191
   ::::::::::::::::::::
Db 871 TACAACCTGATCTCTCATCAAGCTTCCACCTGAGGTTCTTTACGCCCTTCTCAAC 930
QY 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
   ::::::::::::::::::::
Db 931 GTCACTCTTCTTAACCTACAGATCTACCTGAACATCCAGAGCGGACCGGCTCGGGCTG 990
QY 200 ----- 200
Db 991 GATGGGCTCGAGAGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1050
QY 201 -----TrpSerLeuTrpLysArgIleValLeuSerArgCysProSerHis 215
   ::::::::::::::::::::
Db 1051 CCACCGCTGTGCTGGGCTGCTGCGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1110
QY 216 -----AlaGlyPheSerThrThrSerSer 223
   ::::::::::::::::::::
Db 1111 AGGTATGGGCTGGGAGAGCGGCGGTAGCGCTGAGCGGCGGCGGAGCGCACTTCGGGGGT 1170
QY 224 SerAlaSerGlyHisIleuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
   ::::::::::::::::::::
Db 1171 GCGCGTGGGGG-----GCTCCGTGCTTCAACCCACTCCAGCTCCGCGG----- 1215
QY 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgAlaGlyLysSerSerIleLeuVal 263
   ::::::::::::::::::::
Db 1216 -----ACGCTCTCGAGGCGCACTGAGAGCGCGG----- 1245
QY 264 SerLeuArgThrHisMetLeuSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
   ::::::::::::::::::::
Db 1246 -----TCATCTAAGAGGCGCTCCAGCGCTCG 1272
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Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 1273 GCGCTCCGGGCTCAGTGGAGAGCCGATGAAGTGTGCCAGAGCTTCACCCAGCGC 1332
Qy 295 AlGluLeuLeuArgGlyArgGlyLeuAlaArgSerLeuAlaIleLeuSerAlaPhe 314
Db 1333 TTTCGGCTGTCTCCGGGAGAGAAAGTGGCCAAAGTCGTGGCCGCTCATCTGAGCATCTTT 1392
Qy 315 AlaIleCysThrPheAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1393 GGGCTCTGGTGGGCGCCATACCGCTGTATGATCAATCCGGGCGCCTGCCATGGCCAC 1452
Qy 335 GluArgProLysSerValTyrTyrSerIleLeuPheTrpLeuGlnTyrPheAsnSerPhe 354
Db 1453 TGGGTCTCT---GACTACTGGTACGAAACCTCTTCTGGCTCCGTGGGCCAATCGGCT 1509
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnValAlaPheTyrPheIle 374
Db 1510 GTCAACCTGTCTCTCACTCTGTGACACACAGCTTCGCGGGCTTCACCCAGCTG 1569
Qy 375 LeuCysValThrIys-----Trp----- 380
Db 1570 CTCTGCCCCAGAGCTCAAAATCCAGCCCAAGCTCTCTGAGCACTGTGSAAGTGA 1629
Qy 381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db 1630 GTGGCCACGAGAGCTCTCCCTCAGCCAGCTCTCTCAGCCCAAGTCT 1677

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RESULT 4  
US-08-985-090-1  
Sequence 1, Application US/08985090  
Patent No. 5885893  
GENERAL INFORMATION:

APPLICANT: Andrew D.J. Goodearl  
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,090  
FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jean M. Silverl

REGISTRATION NUMBER: 39,030

REFERENCE/DOCKET NUMBER: NMT-032

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2689 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

NAME/KEY: CDS

LOCATION: 291..1625

US-08-985-090-1

Alignment Scores:

Pred. No.:	4,876-65	Length:	2689
Score:	724.50	Matches:	171
Percent Similarity:	48.90%	Conservative:	52
Best Local Similarity:	37.50%	Mismatches:	118
Query Match:	35.38%	Indels:	115
DB:	2	Gaps:	12

US-10-626-445-8 (1-391) x US-08-985-090-1 (1-2689)

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Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
Db 399 CTGGCGCGCTCATGCGCTGCTCATCTGGCCAGCGTGTGGCCAGCGGCTGATG 458
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheAsnLeu 57
Db 459 CTGGCTTCTGTGGCCGAGCTGAGCTCCGACCCAGAACAACTTCTCTGCTCAACCTC 518
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 519 GCCATCTCGACCTTCTCGTGGCGGCTTGTGATCCACTGATGATGACCTGATGCTG 578
Qy 78 Phe---AsnTyrAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 579 ACAGGCGCTGAGACTTCCGCGCGGCTCTGCAAGCTGTGGTATGAGCACTACCTG 638
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 639 CTGTGACCTCTCTCTGCTTCAACATGTGCTCATGACTACAGACCTTCTGTGCTG 658
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 699 ACCGAGCGGTCTCATACCGGCGCCAGAGGTGACACGCGGCGGAGCGGAGAGATG 758
Qy 137 ValAlaValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 759 CTCTGTGTGGTGTGCTGCTGCTTCTGCTGATGAGACAGCCATCTCTG-----AGC 809
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 810 TGGAGAGACTGTCCGGGCGGAGCTCAATCCGAGGCGCACTGATGCGGACTTCTTC 869
Qy 172 ThrGluTyrTyrIleLeuThrIleThrMetLeuGluPheLeuProValIleSer 191
Db 870 TACAAGTGTACTTCTCATACAGGCTTCACCTGAGATTCTTACGCTTCTTCAGC 929
Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 930 GTCACTTCTTAACTCAGACATCTACCTGATCATCCAGAGGCGCACCCGCTCCGCTG 989
Qy 200 ----- 200
Db 990 GATGGGCTCGAGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1049
Qy 201 -----TrpSerLeuTyrLysArgAlaLeuSerArgCysProSerHis 215
Db 1050 CCAACCGCTGTGCTGGGCTGTGTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGC 1109
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 1110 AGGTATGGGTGGGTGAGGCGGCGGCTAGAGGCTGAGGCGGCGGAGGAGGAGGAGGAG 1169
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 1170 GGGCGGTGGGGG-----GGCTCGGTGGCTTACCCACCTCCAGCTCGGCGG--- 1214
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 1215 -----AGCTCTCGAGGCGGCACTGAGAGGCGGCGG----- 1244
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283

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Db      1245 -----TCACTCAAGAGGGGCTCCAAGCCGTCG 1271
QY      284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db      1272 GGGTCTCGGCTGCTGCTGAGAGAGCGCATGAGATGCTGTCCAGAGCTTCAACCCAGCCG 1331
QY      295 AlaGluLeuLeuArgGlyArgGlyLeuAlaArgSerLeuAlaLeuLeuSerAlaPhe 314
Db      1332 TTTCGGCTCTCTCGGACAGAGAAAGTGGCAAGTCCGCTGCGCTCATCTGAGACATCTT 1391
QY      315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThyTyrProArgThr 334
Db      1392 GGGCTCTGCTGGGCCCCCATACAGCTGCTGATGATCATCGGAGCCGCTGCATGGCCAC 1451
QY      335 GluArgProLeuSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheLeuSerPhe 354
Db      1452 TGGCTGCTCT--GACTACTGCTGACGAAACCTCTTCTGCTGCTGCGGCCCAACTGGCT 1508
QY      355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnIleValAlaPheTrpVal 374
Db      1509 GTCAACCTGCTGCTCTCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1568
QY      375 LeuCysValThrLys-----Trp----- 380
Db      1569 CTCTGCCCCCAGAGAGCTCAAAATCCAGCCCCCAGAGCTCCCTGGAGACATGCTGAAGTGA 1628
QY      381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db      1629 GTGGCCCAACAGAGCTCCCTGAGCCAGCCGCTCTCTCAAGCCAGGCTCT 1676

US-09-165-543-1
; Sequence 1, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: NMI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: 291..1625
US-09-165-543-1
Alignment Scores:
Pred. No.: 4,876-65
Score: 724.50
Percent Similarity: 48.90%
Best Local Similarity: 37.50%
Query Match: 35.38%
DB: 3
Gaps: 12

US-10-626-445-8 (1-391) x US-09-165-543-1 (1-2689)
QY      18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIle 37
Db      399 CTGGCCGCGCTATGCGCTGCTCATCTGTGCGACGCGTGGGCAAGCGCTGCTGCTCAAG 458
QY      38 LeuAlaPheValAlaAspArgAsnLeuAlaArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db      459 CTGGCTTCTGCTGGCGGACCTGAGCTCCGACCCAGAACAACTTCTCTGCTCAACCTC 518
QY      58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db      519 GCCATCTCCGACTTCTGCTGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 578
QY      78 Phe---AsnTyrAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db      579 ACAGGCCCTGACCTTCCGCGCGCGCTGCTGCAAGCTGTGCTGTGTGTGCTGCTGCTGCTG 638
QY      97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db      639 CTGTGACCTCTCTGCTGCTTCAACATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 698
QY      117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db      699 ACCCGAGCGGCTCATACCGGCGCAGAGGCTGACACCGCGCGGCGAGCTGCGGAAGATG 758
QY      137 ValAlaValIleTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db      759 CTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 809
QY      157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db      810 TGGAGTACCTGTCCGGGGGAGCTCCATCCCGAGGGCCACTGCTATGCGAGTTCTTC 869
QY      172 ThrGluTyrIleLeuThrIleThrMetLeuGlnIlePheLeuProValIleSer 191
Db      870 TACAACGTGTACTTCTCATACAGGCTTCCACCTGAGGTTCTTAACGCCCTTCTCTCAGC 929
QY      192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db      930 GTCACTTCTTAACTGACATCTAATCTGAACATCCAGAGCGCACCGGCTCCGGCTG 989
QY      200 ----- 200
Db      990 GATGGGCTCAGAGAGCGCGCGCCGAGCCCTCCGAGGCCACCTCACCACCC 1049
QY      201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db      1050 CCACGCGCTGCTGCTGCGCTGCTGCGCAGAGGCGCAGGGAGGAGCCATCGCTGAC 1109
QY      216 -----AlaGlyPheSerThrThrSer 223
Db      1110 AGGTATGGGCTGGCTGAGAGCGCGCTAGCGCTGAGGCTCGGAGGCGAAGCTCGGGGCT 1169
QY      224 SerAlaSerGlyHisLeuHisArgAlaGlyAlaCysArgThrSerAsnProGlyLeu 243
Db      1170 GCGCGTGGGGC-----GCTCCGCTGCTTCAACCACTTCAAGCTCGGC--- 1214
QY      244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db      1215 -----ACCTCTCAGAGGGGCACTGAGAGCGCGC----- 1244

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Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLeuValGlySerPheTrpArg 283  
Db 1245 -----TCACGCAAGAGGGCTCCAAAGCCGTGG 1271  
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294  
Db 1272 GCGCTCCGCGCTCCTACGAGAGAGCCGATGAGATGTCCTCCAGAGCTTCACCCAGCCG 1311  
Qy 295 AlaGluLeuLeuArgGlyArgGlyLeuAlaArgSerIleAlaIleLeuLeuSerAlaPhe 314  
Db 1332 TTTCGGCTGCTCTCGGACAGAGAAAGTGACGAGTCGGCGCTGATCGATCGAGCATCTTT 1391  
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334  
Db 1392 GGGCTCTGCTGGGCGCCATACAGCTGTGATGATCATCCGGCGCGCTGCATGGCCAC 1451  
Qy 335 GluArgProLysSerValITrpyrSerIleAlaPheTrpLeuGlnITrPheAsnSerPhe 354  
Db 1452 TGGCTCCCT---GACTACTGGTACGAAACCTCTTCGGCTCTCTGGGCGCCACTCGGCT 1508  
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374  
Db 1509 GTCAACCTCTGCTCTCTACCTCTGTGCAACCAAGCTTCGCGGGCTTCACCAAGCTG 1568  
Qy 375 LeuCysValThrLys-----Trp-----380  
Db 1569 CTCTGCGCCCGAAGGCTCAAAATCCAGCCCGACAGCTCCCTGAGCACTGCTGGAAGTGA 1628  
Qy 381 -----ProAlaLeuSerGlnAsnGlnSer 388  
Db 1629 GTGGCCACGACAGACCTCTCCACAGCCAGCTCTCTGACGCCAGCTGT 1676

RESULT 6  
US-09-167-354-5  
; Sequence 5, Application US/09167354A  
; Patent No. 6136559  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: JMW  
; CURRENT APPLICATION NUMBER: US/09/167,354A  
; NUMBER FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 2699  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CDNA  
US-09-167-354-5

Alignment Scores:  
Pred. No.: 4.9e-65 Length: 2699  
Score: 724.50 Matches: 171  
Percent Similarity: 48.90% Conservative: 52  
Best Local Similarity: 37.50% Mismatches: 118  
Query Match: 35.38% Indels: 115  
DB: Gaps: 12

US-10-626-445-8 (1-391) x US-09-167-354-5 (1-2699)  
Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37  
Db 407 CTGGCCCGGCTCATGCGGCTCTCATGTCGACAGGTGCGGCAACGCGCTGTATG 466  
Qy 38 LeuAlaPheValValaPargAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57  
Db 467 CTGGCTTCTGTGGCGGACTCGAGCCTCGGACCCAGAAACAACCTTCTCTGCTCACTC 526

Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77  
Db 527 GCCATCTCCGACTCTCTCTGTCGGCGGCTTGTGATCCCATGTATGATACCTTCAGTCTG 586  
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96  
Db 587 ACAGCCGCTGACCTTCGGCGCGGCGCTGTCAACCTGTGGCTGTGAGGACTACTCTG 646  
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrTrpAspArgTyrGlnSerVal 116  
Db 647 CTGGACCTCTCTCTGCTCAACATGTGCTATGACTACAGACGACGCTCTCTGCTG 706  
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136  
Db 707 ACCGAGCGGCTCATACCGGGCCGACAGGGAGACACCGGGGGGAGTGGGAAGATG 766  
Qy 137 ValAlaValITrpleuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156  
Db 767 CTGCTGTGTGGTGTGGCTGCGCTCTCTGTGTACGACAGCCATCTCTG-----AGC 817  
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysAspGluProGlyPheVal 171  
Db 818 TGGAAGTACCTGTCCGGGGGACCTCCATCCCGAAGGCCACTGTATGCCAGTCTTC 877  
Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuGluPheLeuLeuProValIleSer 191  
Db 878 TACACTGTGACTCTCTCATACAGGCTTCACGCTTGAGTCTTTACGCCCTCTCTCAGC 937  
Qy 192 ValAlaTyrPheAsnValGlnIleTyr-----200  
Db 938 GTACACTCTTTAATCTACAGCATCTTACTGATCATCAGAGGCGCAACCGCTCGGCTG 997  
Qy 200 -----200  
Db 998 GATGGGCTTCGAGAGCGAGCGGCCCGGAGCCCTCCGAGGCCACGCTTACCAACCC 1057  
Qy 201 -----TrpSerLeuTyrLysArgArgAlaLeuSerArgCysProSerHis 215  
Db 1058 CCACCGCTGCTGCTGGGCTGTGCGGCTGCGACAAAGGGAGCGGGAGCGGCAACCGCTGAC 1117  
Qy 216 -----AlaGlyPheSerThrThrSerSer 223  
Db 1118 AGGTATGGGTGGGTGAGCGCGCGCTGAGCGCTGAGCGCGGGAGCGGACCTCTCGGGGT 1177  
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243  
Db 1178 GCGGCTGGGGGCT-----GGCTCGGTGGCTTCACCCACTCTCAAGCTCCGGC--- 1222  
Qy 244 LysGluSerAlaIleSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263  
Db 1223 -----AGCTCTCGAGGGGCACTGAGAGGCCCGC-----1252  
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLeuValGlySerPheTrpArg 283  
Db 1253 -----TCACTCAAGAGGGGCTCCAGCCGCTG 1279  
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294  
Db 1280 GCGTCTCTGGCTCTCGCTGGAAGCGGATGAGATGTCCTCCAGAGCTTCACCCAGCCG 1339  
Qy 295 AlaGluLeuLeuArgGlyArgGlyLeuAlaArgSerIleAlaIleLeuSerAlaPhe 314  
Db 1340 TTTCGGCTGCTCTCGGACAGAGAAAGTGCCAAATCCTGCTGCGCTCATCGTGAACATCTT 1399  
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334  
Db 1400 GGGCTCTGCTGGGCGCCATACAGCTGTGATGATCATCGGCGCGCTTCCATGGCCAC 1459  
Qy 335 GluArgProLysSerValITrpyrSerIleAlaPheTrpLeuGlnITrPheAsnSerPhe 354  
Db 1460 TGGCTCCCT---GACTACTGGTACGAAACCTCTTCTGCTCTCTGTGGGCAACTCGGCT 1516

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Qy 355 ValaenProPheLeuTyPProLeuCyvhiarGargPheGlnLysAlaPheTrrpLysIle 374
Db 1517 GTCAACCCCTGCTCTACCTCTGTGGCCACCAAGCTTCGCGGGCCCTTACCAAGAGCTG 1576
Qy 375 LeuCyvAlThrLys-----ProAlaLeuSerGlnAngLysSer 380
Db 1577 CTCTCCCCCAGAGACTCAAAATCCAGCCCCAGAGCTCCCTGAGACACTGTGGAAGTGA 1636
Qy 381 -----Trrp-----
Db 1637 GTGGCCCAACAGAGCTCCCTCAGCCAGCCCTCTCAGCCCAAGGTCT 1684

RESULT 7
US-09-642-855-5
; Sequence 5, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyaeli, Jayashree
; APPLICANT: Huvax, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; SUBTYPE
; FILE REFERENCE: NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-5

Alignment Scores:
Pred. No.: 4.9e-65 Length: 2699
Score: 724.50 Matches: 171
Percent Similarity: 48.90% Conservatave: 52
Best Local Similarity: 37.50% Mismatches: 118
Query Match: 35.38% Indels: 115
Gaps: 12

US-10-626-445-8 (1-391) x US-09-642-855-5 (1-2699)
Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
Db 407 CTGGCCCGGCTCAATGCGCTGCTCATCTGGCCACGCTGGGCAAGCGCTGCTCATG 466
Qy 38 LeuAlaPheValAlaAspArgAsnLeuAlaGhiAsrSerAsnTyPhePheLeuAlaLeu 57
Db 467 CTCGCTTCGCGGCGGCTGCGAGCTCCGACCCAGAACAACTTCTCTGCTCAACTC 526
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIlePProLeuTyPheProHisValLeu 77
Db 527 GCCATCTCCGACTCTCTGCTGCGCGCTTCGTCATCCCACTGATGATCCCTACGCTG 586
Qy 78 Phe---AsnTrrpAsnPheGlySerGlyIleCysMetPheTrrpLeuIleThrAspTyLeu 96
Db 587 ACAGCGCCCTGACCTTGGCGGGGCTCTGCAAGCTGTGGCTGTGTGACTACCTG 646
Qy 97 LeuCyvAlThrAlaSerValTyAsnIleValLeuIleSerTyAspArgTyGlnSerVal 116
Db 647 CTGTGCACTCTCTGCTGCTTCAACATCGTGTCACTACGACCGCTTCTGCTGCTG 706
Qy 117 SerAsnAlaValSerTyArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 707 ACCGAGGCTCTCTATACCGGCGCCAGAGGTGACACGCGCGGAGTGGGGAAGTGTG 766
Qy 137 ValAlaValTrrpIleLeuAlaPheLeuValAsnGlyPProMetIleLeuAlaSerAspSer 156

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Db 767 CTGCGTGTGGGTGCTGCTGCTCTCTGCTGACGAGACCATCTCTG-----AGC 817
Qy 157 TrrpLys-----AsnSerThrAsnThrLysAspCyvGlnProGlyPheVal 171
Db 818 TGGAGTACTCTGCTCGGAGGAGCTCATCCCGAGGCGCACTGTATGCCAGTCTTCTC 877
Qy 172 ThrGlnTrrpTyPheLeuThrIleThiMetLeuGlnPheLeuProValIleSer 191
Db 878 TACAATGATCTTCTTATACAGGCTTCCACCCGTGAGTCTTTAGCCCTTCTCTACG 937
Qy 192 ValAlaTyPheAsnValGlnIleTy-----
Db 938 GTCACTTCTTTAACCCTAGACATCTGAACATCCAGAGGCGACCCGCTCGGCTG 997
Qy 200 -----
Db 998 GATGGGCTCGAGAGCAGCGGCGCCGAGCCCTCCGAGGCCACCCCTACACACC 1057
Qy 201 -----TrrpSerLeuTrrpLysArgAlaLeuSerArgCyvProSerHis 215
Db 1058 CCACCGCTGCTGCTGGGCTGCTGCTGCGAGAGGCGCAGGAGGCGCATGCGCTGCAC 1117
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 1118 AGGTATGGCGTGGTGAAGCGGCGGCTGAGCGCTGAGCGGCGGAGCGACCTCGGGGT 1177
Qy 224 SerAlaSerGlyNHsLeuNHsArgAlaGlyValAlaCyvArgThrSerAsnProGlyLeu 243
Db 1178 GCGCGTGGGGGCG-----GGCTCCGTGGCTTACCCACCTCCAGCTCCGCGGCG--- 1222
Qy 244 LysGlnSerAlaAlaSerArgHisSerGlnSerProAlaGlyLysSerSerIleLeuVal 263
Db 1223 -----ACCTCTCGAGGCGCACTAGAGCGCGCGC----- 1252
Qy 264 SerLeuArgThrNHsMetLeuAsnSerSerIleThrAlaPheValGlySerPheTrrpArg 283
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Qy 284 SerGlnSerAlaAlaLeuArgGlnArg-----GlnTyP 294
Db 1280 GCGTCTGCTGGCTGCTGCTGAGAACGCGCATGAGATGTGTGCCAGAGCTTCCACCGAGCGC 1339
Qy 295 AlaGlnLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1340 TTTGCGCTGCTCGAGACAGGAAAGTGGCCAAAGTGGCTGGCGCTGTCATCTGATGATCTT 1399
Qy 315 AlaIleCyvTrrpAlaProTyCyvLeuPheThrIleValIleLeuSerThrTyProArgThr 334
Db 1400 GGGCTGCTGCGGCGCCATACAGCTGTGTATGATCATCCGGGCGGCTGCGCATGGCCAC 1459
Qy 335 GlnArgProLysSerValTrrpTySerIleAlaPheTrrpLeuGlnTrrpAsnSerPhe 354
Db 1460 TGCGTCCCT---GACTAGTGTACGAAACCTCTTCTGGCTCGTGGGCGCACTCGGCT 1516
Qy 355 ValaenProPheLeuTyPProLeuCyvhiarGargPheGlnLysAlaPheTrrpLysIle 374
Db 1517 GTCAACCTGCTCTTACCTCTGCTGCGACACAGCTTCGCGGGCCCTTACCAAGAGCTG 1576
Qy 375 LeuCyvAlThrLys-----ProAlaLeuSerGlnAngLysSer 380
Db 1577 CTCTCCCCCAGAGCTCAAAATCCAGCCCCAGAGCTCCCTGAGACACTGTGGAAGTGA 1636
Qy 381 -----Trrp-----
Db 1637 GTGGCCCAACAGAGCTCCCTCAGCCAGCCCTCTCAGCCCAAGGTCT 1684

RESULT 8
US-09-642-514-5
; Sequence 5, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy

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/ APPLICANT: Exlander, Mark  
 / APPLICANT: Pyacti, Jayashree  
 / APPLICANT: Huvart, Arne  
 / TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
 / TITLE OF INVENTION: SUBTYPE  
 / FILE REFERENCE: ORT1290  
 / CURRENT APPLICATION NUMBER: US/09/642,514  
 / CURRENT FILING DATE: 2000-08-21  
 / PRIOR APPLICATION NUMBER: US 09/167,354  
 / PRIOR FILING DATE: 1998-10-06  
 / NUMBER OF SEQ ID NOS: 8  
 / SOFTWARE: PatentIn Ver. 2.0  
 / SEQ ID NO 5  
 / LENGTH: 2699  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Description of Artificial Sequence: CDNA  
 / US-09-642-514-5

Alignment Scores:  
 Pred. No.: 4.9e-65 Length: 2699  
 Score: 724.50 Matches: 171  
 Percent Similarity: 48.90% Conservative: 52  
 Best Local Similarity: 37.50% Mismatches: 118  
 Query Match: 35.38% Indels: 115  
 Gaps: 12

US-10-626-445-8 (1-391) x US-09-642-514-5 (1-2699)  
 QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIle 37  
 Db 407 CTGGCCCGGCTGATGCGGCTGCTCATGTCGCGCCACGCGTGGCAACGCGGCTGATG 466  
 QY 38 LeuAlaPheValAlaPheArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57  
 Db 467 CTGCGCTTCGTGGCGGCTGCTGCTGCGACCCGACCAACTTCTTCTGCTCAACTC 526  
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 Db 527 GCGATCTCCGACTCTGCTGCTGCGGCTTCTGCACTCCAGTATGATGATCGTCTG 586  
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 Db 587 ACAGCGCGCTGACCTTCCGCGCGGCTCTGCAAGCTGTGCGTGAAGTGAATCTG 646  
 QY 97 LeuCySerThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116  
 Db 647 CTGTGCACTCTCTGCTGCTCAACATGCTGCTCATGACTACGACCCGCTTCTGCTG 706  
 QY 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMet 136  
 Db 707 ACCGACCGGCTCTATACCGGCGGACAGGCTGACACCGCGCGGACGCGGAGATG 766  
 QY 137 ValAlaValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156  
 Db 767 CTCTGTGTGGGTGGTGGCTTCTCTCTGTCAGCGACCAAGCACTCG-----AGC 817  
 QY 157 TrrPyr-----AsnSerThrAsnThrLysAspCysGlnProGlyPheVal 171  
 Db 818 TGGAGTACCTGTCCGCGGCGGACCTCATCCCGAGGCGCACTGCTATGCCGATTCTTC 877  
 QY 172 ThrGlnTrrPyrIleLeuThrIleThrMetLeuGlnIupheLeuProValIleSer 191  
 Db 878 TACACGTGTGACTTCTCATACGCGCTTCAACCTGAGTCTTTACGCGCTTCTCAGC 937  
 QY 192 ValAlaTyrPheAsnValGlnIleTyr----- 200  
 Db 938 GTCACTTCTTTAACTTCAGACATCTAATCAATCCAGAGCGCCACCGCTCCGCGCTG 997  
 QY 200 ----- 200  
 Db 998 GATGGGCTCGAGAGCGCGCGCGCGCGCGCTCCCGAGGCGCCAGCTTCACACCC 1057

QY 201 -----TrrSerLeuTrrPyrArgArgAlaLeuSerArgCysProSerHis 215  
 Db 1058 CCACCCGCTGCTGCTGCGGCTGCTGCTGCGAGAGCGGACCGGAGCGCATGCCGCTGCAC 1117  
 QY 216 -----AlaGlyPheSerThrThrSerSer 223  
 Db 1118 AGGTATGGGTGGGTGAGCGCGCTGAGCGCTGAGAGCGGAGCGGAGCGGAGCTTCGGGAGGT 1177  
 QY 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243  
 Db 1178 GCGGTGGGGC-----GGCTCCGTGGCTTCAACCCACTCCAGCTCCGCGC--- 1222  
 QY 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263  
 Db 1223 -----AGCTCTCGAGGGGCACTGAGAGCGCGC----- 1252  
 QY 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValAlaSerPheTyrArg 283  
 Db 1253 -----TCACTCAAGAGGGCTTCAAGCGCTCG 1279  
 QY 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294  
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 QY 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuSerAlaPhe 314  
 Db 1340 TTTCGGCTGTCTCGGACAGAGAAAGTCCCAAGTCCCTGCGCTCATCGTGAACATCTTT 1399  
 QY 315 AlaIleCysTrrAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334  
 Db 1400 GGGCTCTGCTGGGCGCCCATACACGCTGATGATGATCATCGCGCGCTGCCATGCGCAC 1459  
 QY 335 GluArgProLysSerValTrrPyrSerIleAlaPheTrrLeuGlnTrrPheAsnSerPhe 354  
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 QY 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnValAlaPheTrrPyrIle 374  
 Db 1517 GTCAACCTGTCTCTTACCTCTGTGTCCACACAGCTTCGCGCGGCTTCAACCAAGCTG 1576  
 QY 375 LeuCysValThrLys-----Trr----- 380  
 Db 1577 CTCTGCCCGCAGAAAGCTCAAAATCCAGCCCAAGCTCCCTGAGCACTGTGGAATGTA 1636  
 QY 381 -----ProAlaLeuSerGlnAsnGlnSer 388  
 Db 1637 GTGGCCACACAGACCTCTCTCAGCCAGCGCTCTTCAAGCCGAGTCT 1684  
 RESULT 9  
 US-08-985-090-3  
 / Sequence 3, Application US/08985090  
 / Patent No. 5885893  
 / GENERAL INFORMATION:  
 / APPLICANT: Andrew D. J. Goodearl  
 / TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR  
 / NUMBER OF SEQUENCES: 28  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 / STREET: 28 State Street  
 / CITY: Boston  
 / STATE: Massachusetts  
 / COUNTRY: USA  
 / ZIP: 02109  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / FILING DATE:  
 / APPLICATION NUMBER: US/08/985,090  
 / PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jean M. Silveri  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: MNI-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1335 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1335  
US-08-985-090-3  
Alignment Scores:  
Pred. No.: 2,56-65 Length: 1335  
Score: 722.50 Matches: 165  
Percent Similarity: 50.82% Conservative: 51  
Best Local Similarity: 38.82% Mismatches: 116  
Query Match: 35.28% Indels: 93  
DB: 2 Gaps: 10  
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QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIle 37  
DB 109 CTGGCGCGCTATGAGCGCTGCTCATCGGCGCAGGCTGAGCAACCGCTGGTCAAG 168  
QY 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57  
DB 169 CTGGCTTCGTGGCGGAGCTCGAGCGCTCGGCGCAGAGAACACTTCTCTGCTCAACCTC 228  
QY 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77  
DB 229 GCCATCTCGAGCTTCTGCTCGGCGCTTCTGCACTCCCACTGATGATCCCTACGCTCG 288  
QY 78 Phe---AsnTyrAsnPheGlySerGlyIleCysMetPheTyrPheLeuIleThrAspTyrLeu 96  
DB 289 ACAGCGCGCTGAGCTTGGCGCGGCGCTCTGCAAGCTGTGGTGGTGAAGTAACTCG 348  
QY 97 LeuCyThrAlaSerValTyrAsnIleValIleIleSerTyrAspArgTyrGlnSerVal 116  
DB 349 CTGTGCACCTCTCTGCTCAACATCGTCAATCAGTCAAGTCAAGCGCTCTCTGCTGTC 408  
QY 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLeuIleValAlaGlnMet 136  
DB 409 ACCCGAGGGGTCTCTACCGGCGCCAGCGGTGACACCGCGGCGGAGTGGGAATG 468  
QY 137 ValAlaValTyrPheLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156  
DB 469 CTGCTGGTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519  
QY 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171  
DB 520 TGGGAGTACCTGTCCGGGGGAGCTCCATCCCGAGGGGCACTGCTAAGCCAGTTCTTC 579  
QY 172 ThrGluTyrTyrIleLeuThrIleThrMetLeuGluPheLeuLeuProValIleSer 191  
DB 580 TACAACCTGATCTTCTCATCAAGGCTTCCACCTGAGATTCTTAAACCCCTTCTCAGC 639  
QY 192 ValAlaTyrPheAsnValGlnIleTyr----- 200  
DB 640 GTCACTTCTTAACTCAAGCATCTTAACATCAAGAGGCGACCCGCTCGGCTG 699  
QY 200 ----- 200

DB 700 GATGGGCTCGAGAGCAGCCGCCGAGCCCTCCCGAGGCCAGCCCTCAACACC 759  
QY 201 -----TyrSerLeuTyrPheArgAlaLeuSerArgCysProSerHis 215  
DB 760 CCACCGCTGTGCTGGGCTGTGCGAGAGGGGACGGGGAGGCCCATGCGCTGCAC 819  
QY 216 -----AlaGlyPheSerThrHisSerSer 223  
DB 820 AGGTATGGGGTGGGAGCGCCCGCTAGCCCTGAGCCCGGGAGGCCACCTCGGGGT 879  
QY 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243  
DB 880 GGCGGTGGGGC-----GGCTCCGTGGCTTCAACCACTTCCAGCTCCGGC--- 924  
QY 244 LysGluSerAlaAlaSerArgHisSerGluSerProAlaGlyLysSerSerIleLeuVal 263  
DB 925 -----AGCTCTCGAGGGGCACTGAGGCGCGC----- 954  
QY 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTyrArg 283  
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QY 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294  
DB 982 GCGTCTCGGCTCTCACTGAGAGAGCATGAAGATGTGTCCAGAGCTTCAACCGAGCC 1041  
QY 295 AlaGluLeuLeuArgGlyArgGlyLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314  
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QY 315 AlaIleCysTyrAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334  
DB 1102 GCGCTCTCTGCGCCCTCAACAGCTGCTGATGATCACTCGGCGCGCTCCAGCCAGC 1161  
QY 335 GluArgProLysSerValTyrTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerPhe 354  
DB 1162 TGGCGCT---GACTACTGAGAGCAACCTCTTCTGCTGCTGTGGCCAACTCGGCT 1218  
QY 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysValaPheTyrValle 374  
DB 1219 GTCAACCTGTGCTCTTACCTCTGTGCGACCAAGCTTCCGCGGCTTCAACCAAGCTG 1278  
QY 375 LeuCysValThrLys 379  
DB 1279 CTCTGCCCCAGAG 1293  
RESULT 10  
US-09-165-543-3  
Sequence 3, Application US/09165543  
Patent No. 6093545  
GENERAL INFORMATION:  
APPLICANT: Andrew D.J. Goodearl and Sandra Gluckeman  
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/165,543  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,780  
FILING DATE:









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QY 200 ----- 200
DB 700 GATGGGGCTGAGAGGACGGCCCGGAGCCCTCCGAGGCCACCCCTCACACC 759
QY 201 -----TTPSerLeuTPrlyAArgAlaLeuSerAArgCyAProSerHis 215
DB 760 CCACGGCTGCGCTGGGGCTGCTGGCAAGAGGGGACGGGAGGCCATGCGCTGCAC 819
QY 216 -----AlGlyPheSerThrThrsSer 223
DB 820 AGGTATGGGTGAGTGAAGCGCGCGCTAGCGCTGAGCGGGGAGCGGACCTCGGGGGT 879
QY 224 SerAlaSerGlyHisLeuHisAArgAlaGlyValAlaCyAArgThrsSerAProGlyLeu 243
DB 880 GCGCGTGGGGG-----GGCTCCGTGGCTTCAACCACTCCGCTCGGC--- 924
QY 244 LySGLuSerAlaAlaSerAArgHisSerGluSerProAArgAArgLySerSerHisLeuVal 263
DB 925 -----AGCTCTCGAGGGGCACTGAGAGGCCCGC----- 954
QY 264 SerLeuAArgThrHisMetAAsnSerSerIleThrAlaPheLeuValGlySerPheTrpArg 283
DB 955 -----TCACATCAGAGGGGCTCCAAGCGCGT 981
QY 284 SerGluSerAlaAlaLeuAArgGlnArg-----GluTyr 294
DB 982 GGGTCTCGGCTCGCTGGAGAGCGCATGAAGATGCTGCCAGAGCTTCAACCCAGCGC 1041
QY 295 AlaGluLeuLeuAArgGlyAArgLySerLeuAlaArgSerLeuAlaIleLeuSerAlaPhe 314
DB 1042 TTTCGGCTGTCTCGGACAGGAAGTGGCAAGTCCGCTGCGCTACGTCAGCATCTT 1101
QY 315 AlaIleCyAArgTPrlyAProTyrCyALeuPheThrIleValLeuSerThrTyrProAArgThr 334
DB 1102 GGGCTCTGGGGCCCATACACAGCTGATGATCATCGGGGCGCTGCATGGCCAC 1161
QY 335 GluAArgProLySerValTPrlySerIleAlaPheTrpLeuGlnTrpPheAAsnSerPhe 354
DB 1162 TGGCTCCCT--GACTACTGTGACGAAACCTCTTGGCTCTGCGGCCCAACTCGGCT 1218
QY 355 ValAAsnProPheLeuTyrProLeuCyAHisAArgAArgPheGlnValAlaPheTrpLySile 374
DB 1219 GTCAACCTGTCTCTTACCTCTGTGCGCACACAGCTTCCGCGGCGCTTCAACAGCTG 1278
QY 375 LeuCyAValThrLyS 379
DB 1279 CTCTGCCCCCAGAG 1293

RESULT 14
US-09-891-053-21
; Sequence 21, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hitaru
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masaaki
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yunsuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/45661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 2050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271)..(1629)
US-09-891-053-21

Alignment Scores:
Pred. No.: 5,05e-65 Length: 2050
Score: 722.50 Matches: 165
Percent Similarity: 50.82% Conservative: 51
Best Local Similarity: 38.82% Mismatches: 116
Query Match: 35.28% Indels: 93
DB: 4 Gaps: 10

US-10-626-445-8 (1-391) x US-09-891-053-21 (1-2050)
QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAAsnAlaValAlle 37
DB 379 CTGGCGGCGCTCATGCGCTCATGCGTGGCGACGAGTGGCGGACGCGCTGTCACATC 438
QY 38 LeuAlaPheValAlaAArgAAsnLeuAArgHisAArgSerAAsnTyrPhePheLeuAAsnLeu 57
DB 439 CTGGCTTGTGAGCGGACCTCGAGCTCGGACCCAGAACAACTTCTCTGCTCAACCTC 498
QY 58 AlaIleSerAAsnPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
DB 499 GCGATCTCGACTTCTCTGTGGCGGCTTTCGATCCACGTATGATACCTACGAGCTG 558
QY 78 Phe---AAsnTPrAsnPheGlySerGlyIleCyAAsnMetPheTrpLeuIleThrAArgTyrLeu 96
DB 559 ACAGCGCGCTGACCTTGGCGGCGCTGTCAGAGCTGTGGCTGTAGTGAATACCTG 618
QY 97 LeuCyAThrAlaSerValTyrAAsnIleValLeuIleSerTyrAAsnAArgTyrGlnSerVal 116
DB 619 CTGTACACTCTCTGCTTCAACATCGTGTCACTGACATGACAGACCTTCTGTGGCTG 678
QY 117 SerAAsnAlaValSerTyrAArgAlaGlnHisThrGlyIleMetLeuIleValAlaGlnMet 136
DB 679 ACCGAGGAGGTCTCATCGGCGCACAGGAGTGAACAGCGCGGCGAGTGGCAAGT 738
QY 137 ValAlaValTPrIleLeuAlaPheLeuValAAsnGlyProMetIleLeuAlaSerAAsnSer 156
DB 739 CTGCTGTGTGGTCTGCTGCTTCTGCTGTGAAGGACGACCATCTG-----AGC 789
QY 157 TPrLyS-----AAsnSerThrAAsnThrLySAsnCyAAsnProGlyPheVal 171
DB 790 TGGAGTACTGTCCGGGGGCGAGCTCATCCCGAGGCGCACTGTATGCCAGTTCTTC 849
QY 172 ThrGluTPrTyrIleLeuThrIleThrMetLeuLeuGluPheLeuProValIleSer 191
DB 850 TACAACTGTACTTCTCATGACGCTTCAACCTGGAAGTTCTTACGCCCTTCTCTCAC 909
QY 192 ValAlaTyrPheAAsnValGlnIleTyr----- 200
DB 910 GTCACTTCTTAACTCAGATTACTGAACATCAGAGGCGGACCGGCTCGGGCTG 969
QY 200 ----- 200
DB 970 GATGGGCTGAGAGGACGGCCCGGAGCCCTCCGAGGCCACCCCTCACACC 1029
QY 201 -----TTPSerLeuTPrlyAArgAlaLeuSerAArgCyAProSerHis 215
DB 1030 CCACGGCTGCGCTGGGGCTGCTGGCAAGAGGGGACGGGAGGCCATGCGCTGCAC 1089
QY 216 -----AlGlyPheSerThrThrsSer 223
DB 1090 AGGTATGGGTGAGTGAAGCGCGCGCTAGCGCTGAGCGGGGAGCGGACCTCGGGGGT 1149
QY 224 SerAlaSerGlyHisLeuHisAArgAlaGlyValAlaCyAArgThrsSerAProGlyLeu 243

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Db      1150 GGGCGTGGGGC-----GGCTCCGTGGCTTCAACCACTCCAGCTCCGGC--- 1194
Qy      244 LygGlusSerAlaAlaSerArgHisSerGlusSerProArgHisSerSerSerIleVal 263
Db      1195 -----AGCTCTCGAGGGGCACTGAGAGCGCGC----- 1224
Qy      264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheIysValGlySerPheTrpArg 283
Db      1225 -----TCACCTCAAGAGGGGCTCCAGCCCTCG 1251
Qy      284 SerGlusSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db      1252 GCGCTCCCTCGGCTCGCTGAGAGAGCCGATGAAGATGGTGTCCAGAGCTTCAACCAAGCGC 1311
Qy      295 AlaGluLeuLeuArgGlyArgIysLeuAlaArgSerIleValIleLeuLeuSerAlaPhe 314
Db      1312 TTTCGGCTGTCTCGGAGCAGAGAAAGTGCACAGTGGCTGGCGCTCATGAGCATCTTT 1371
Qy      315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db      1372 GGGCTGTGCTGGGCCCCATACAGCTGTCTGATATCATCCGGCGCCGCTCCATGGGCAC 1431
Qy      335 GluArgProIysSerValIleTyrSerIleAlaPheTrpLeuGlnIleTrpPheAsnSerPhe 354
Db      1432 TGGCTCCCT---GACTACTGGTACGAAACCTCTTGTGGCTCTGTGGGCAACTCGGCT 1488
Qy      355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnIysAlaPheTrpIle 374
Db      1489 GTCAACCTCTCTCTTACCTCTGTGTGCACACAGCTTCGCGGGGCTTCAACCAAGCTG 1548
Qy      375 LeuCysValThrIys 379
Db      1549 CTCTGCCCCCAGAG 1563

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RESULT 15
US-09-165-543-6
; Sequence 6, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1338 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-09-165-543-6
Alignment Scores:
Pred. No.      1,06e-64      Length:      1338
Score:         716.50      Matches:      165
Percent Similarity: 53.41%      Conservative: 54
Best Local Similarity: 40.24%      Mismatches: 128
Query Match:    34,99%      Indels:      63
DB:              3      Gaps:      10
US-10-626-445-8 (1-391) x US-09-165-543-6 (1-1338)
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Qy      38 LeuAlaPheValAlaAspArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db      169 CTGCGCTTCTGGCGGATTCGAGCTCCGACCAACAACTCTTCTGCTCAACTC 228
Qy      58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db      229 GCGATCTCCGACTTCTCTCGGGTGCCTTGTGATCCATTCATGACCTTATGCTG 288
Qy      78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db      289 ACCGGCGTTGACCTTCCGCGCGGCGCTGTGCAAGCTGTGGTGTGATGACTCTTA 348
Qy      97 LeuCysThrAlaSerValTyrAsnIleValIleIleSerTyrAspArgTyrGlnSerVal 116
Db      349 CTGTGTGCTCCCTCGGCTTTCACATCTGATCATGATGACGATGACGATTCGTGATG 408
Qy      117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetIysIleValAlaGlnMet 136
Db      409 ACTCGAGCTGTCTCTTACAGAGGCCGACAGGGGGAACAGAGCGGCGCTTGGAAAGATG 468
Qy      137 ValAlaValAlaTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db      469 GCACTGTGTGGTGTGGCTTCTGTGTATGAGGCTGTGCATCTG-----AGT 519
Qy      157 TrpIys-----AsnSerThrAsnThrIlyAspCysGluProGlyPheVal 171
Db      520 TGGAGTACCTGTCTGTGTGACATTCATCCCGAGGGCCCATGTGATGATCTTTC 579
Qy      172 ThrGluTrpTyrIleLeuThrIleThrMetLeuGluPheLeuAsnProValIleSer 191
Db      580 TACAACTGTACTTTTCTCATACAGGCTCCACCTTGAGTTCTTCAAGCCCTTCTCAGC 639
Qy      192 ValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrpIysArgAlaLeu----- 209
Db      640 GTTACCTTCTTCAACTCAGCATCTACGTGAATCATCAGAGGGGCAACCGGCTTCGCTT 699
Qy      210 -----SerArgCysProSerHis 215
Db      700 GATGGGGCCGTGAGGCTGGCCAGAACCCCAACAGATGCCAGCCCTTGCACCTCCA 759
Qy      216 AlaGlyPheSerThrThrSerSerSerAlaSerGlyHis-----LeuHis 230
Db      760 GCTCCCCCAGCTGTCTGGGGCTGTGAGCCAAAGGCAATGGCAAGGCATCCGTTGAC 819
Qy      231 ArgAlaGlyValAlaCysArgThrSerAsnProGlyLeuHis----- 244
Db      820 AGGTATGGGGTGGT-----GAGGCAAGGCTGTGTGAGGCTGGGAGGCTGCCCTC 873
Qy      245 -----GluSerAlaAlaSer 249
Db      874 GGGGCTGGCAGTGTGAGAGTGTGCTGTGCTCCCACTCCAGCTTCAGACTCTCTCA 933

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 6, 2005, 19:35:37 ; Search time 741 Seconds  
(without alignments)  
3197.654 Million cell updates/sec

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Perfect score: 2048  
Sequence: 1 MSESNTGILPPAAQVLA.....WKLCVTKWPAISQNSVSS 391

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5615251 seqs, 3030001701 residues  
Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2\_1/USPTO/US1066445/runac\_06042005\_130824\_9864/app\_query.fasta\_1.583  
-DB=Published Applications NA -QPM=fastcap -SUFFIX=rnpb -MINMATCH=0.1  
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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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Database : Published Applications NA:  
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9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
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16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
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20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2035	99.4	1176	US-10-626-445-5	Sequence 5, Appl
2	1745	85.2	1176	US-10-626-445-6	Sequence 6, Appl
3	1370.5	66.9	1173	US-09-812-216-1	Sequence 1, Appl
4	1370.5	66.9	1173	US-09-910-411-1	Sequence 1, Appl
5	1370.5	66.9	1173	US-09-875-076-13	Sequence 13, Appl
6	1370.5	66.9	1173	US-09-876-252-13	Sequence 13, Appl
7	1370.5	66.9	1173	US-10-052-193-1	Sequence 1, Appl
8	1370.5	66.9	1173	US-10-272-983-13	Sequence 13, Appl
9	1370.5	66.9	1173	US-10-354-769-1	Sequence 1, Appl
10	1370.5	66.9	1173	US-10-393-807-13	Sequence 13, Appl
11	1370.5	66.9	1173	US-10-417-820A-13	Sequence 13, Appl
12	1370.5	66.9	1173	US-10-349-253A-1	Sequence 1, Appl
13	1370.5	66.9	1173	US-10-723-955-13	Sequence 13, Appl
14	1370.5	66.9	1173	US-10-782-596-13	Sequence 13, Appl
15	1370.5	66.9	1173	US-10-737-619-1	Sequence 1, Appl
16	1370.5	66.9	1173	US-10-626-445-1	Sequence 1, Appl
17	1370.5	66.9	1266	US-09-891-138A-5	Sequence 5, Appl
18	1370.5	66.9	1300	US-09-852-165-1	Sequence 1, Appl
19	1370.5	66.9	1300	US-10-626-445-7	Sequence 7, Appl
20	1370.5	66.9	1300	US-10-626-445-7	Sequence 7, Appl
21	1370.5	66.9	1300	US-10-626-445-7	Sequence 7, Appl
22	1366.5	66.7	1265	US-10-225-567A-628	Sequence 628, App
23	1366.5	66.7	1265	US-10-225-567A-628	Sequence 25, Appl
24	1238	60.4	1170	US-10-626-445-7	Sequence 7, Appl
25	724.5	35.4	2689	US-09-350-206-1	Sequence 1, Appl
26	724.5	35.4	2689	US-09-349-755-1	Sequence 1, Appl
27	724.5	35.4	2689	US-09-166-334-1	Sequence 1, Appl
28	724.5	35.4	2689	US-10-282-958-1	Sequence 1, Appl
29	724.5	35.4	2699	US-10-225-567A-548	Sequence 548, App
30	724.5	35.4	2699	US-10-727-021-5	Sequence 5, Appl
31	724.5	35.4	2699	US-10-757-262-131	Sequence 131, App
32	722.5	35.3	1335	US-09-350-206-3	Sequence 3, Appl
33	722.5	35.3	1335	US-09-349-755-3	Sequence 3, Appl
34	722.5	35.3	1335	US-09-166-334-3	Sequence 3, Appl
35	722.5	35.3	1335	US-10-282-958-3	Sequence 3, Appl
36	722.5	35.3	1335	US-10-727-021-6	Sequence 6, Appl
37	722.5	35.3	2050	US-09-891-053-21	Sequence 21, Appl
38	722.5	35.3	2050	US-10-759-463-21	Sequence 21, Appl
39	716.5	35.0	1338	US-09-349-755-6	Sequence 6, Appl
40	716.5	35.0	1338	US-09-349-755-6	Sequence 6, Appl
41	716.5	35.0	1338	US-09-166-334-6	Sequence 6, Appl
42	716.5	35.0	1338	US-10-282-958-6	Sequence 6, Appl
43	716.5	35.0	1953	US-09-891-053-26	Sequence 26, Appl
44	716.5	35.0	1953	US-10-759-463-26	Sequence 26, Appl
45	716.5	35.0	2761	US-10-152-319A-2003	Sequence 2003, Ap

## ALIGNMENTS

RESULT 1  
US-10-626-445-5  
Sequence 5, Application US/10626445  
Publication No. US20040248252A1  
GENERAL INFORMATION:  
APPLICANT: Lovenberg, Timothy  
TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
FILE REFERENCE: PRD-0032  
CURRENT FILING DATE: 2003-07-23  
PRIOR FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: 09/790,849  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: 60/208,260  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 5  
LENGTH: 1176  
TYPE: DNA



ORGANISM: Mus musculus  
US-10-626-445-5

## Alignment Scores:

Prod. No.: 6,42e-215 Length: 1176  
Score: 2035.00 Matches: 390  
Percent Similarity: 99.74% Conservative: 0  
Best Local Similarity: 99.74% Mismatches: 1  
Query Match: 99.37% Indels: 0  
DB: 18 Gaps: 0

US-10-626-445-8 (1-391) x US-10-626-445-5 (1-1176)

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Db 1 ATGTGGAGCTTAACATGCTGATCTTGGCCACCTGCTGAGCTCCCTTGCACTTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTAATGCTTCATTGGCTTGGCTATATGATGATGATGATGATGATGATGATGATGAT 120
Qy 41 ValValAspArgAnSerThrGlyIleLeuProProAlaIleValProLeuAlaPhe 60
Db 121 GTGGTGGACGAAACCTTACACATGAAATATATATATATATATATATATATATATAT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrlleProHisValleuPheAnTrp 80
Db 181 GACTCTCTGCGGTGATTTGATTCATTCCTGACATCCCTGACGCTGTTTAACTGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrlleLeuLeuCythrAla 100
Db 241 AATTTTGAAGTGAATCTGCATGTTTGGCTCATCTACTGATCTTTTGTGACCGCA 300
Qy 101 SerValTyrlleAnIleValIleIleSerTyrlleAspArgTyrlleGlnSerValSerAsnAlaVal 120
Db 301 TCTGCTACATATATGCTTCATTAGCTAGATGAAACAGTTCAGTTCAAAAGCTGTG 360
Qy 121 SerTyrlleArgIleGlnIleSerGlyIleMetCysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTTATGGGCTCAACACCTGSCATCATGAAATGTTGCTCAAAAGCTGTG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160
Db 421 ATACTGCTTCTTGGTAAATGCGCCGATGATCTGCTTCAGATTCCTTGGAGAACAGC 480
Qy 161 ThrAsnThrIleAspPheCysGlnProGlyPheValThrGluTrpTyrlleLeuThrIleThr 180
Db 481 ACGAAACAAAGGACTGTGAGCCGTGCTTGTTCAGAGTGTACATCCCAACATTACA 540
Qy 181 MetLeuLeuGlnPheLeuLeuProValIleSerValAlaTyrllePheAsnValGlnIleTyrlle 200
Db 541 ATGCTCTGGAATTCCTGCTTCTCTGCTCATCTCTGCTTATTTCAATGATGACATTTAC 600
Qy 201 TrpSerLeuTrpIleAspArgAlaIleLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 601 TGAAGCTGAGGAGCGTAAGGCTCTCAGTGTGAGCCCTAGCCATGCTGAGATTCCTCACT 660
Qy 221 ThrSerSerSerAlaSerGlyIleLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 661 ACCCTTCCAGTGTCTTACAGACATTCACAGACCTGCGGTGAGCTTACAGACAAAGTAAT 720
Qy 241 ProGlyLeuIleGlnSerAlaAlaSerArgHisSerGluSerProArgArgIleSerSer 260
Db 721 CTTGAGATTGAGAGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheIleValGlySer 280
Db 781 ATCTGTGGTGTCTTAAAGACTCAATGAAACAGAGTACATGCTTCAAAAGTGGTTC 840
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgIleTyrlleGlnLeuLeuArgGly 300
Db 841 TTCTGGGATCGGAAGTGCAGCCTTGCCTCAAAAGGAGTACAGGAGGCTTCTCAGAGGC 900

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Qy 301 ArgIleLeuAlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGGAGCTAGCCAGCTACATGCGCATCTTCTGAGCGCTTTTCCATTTCTGGGCTCCA 960
Qy 321 TyrCysLeuPheThrIleValleuSerThrTyrlleProArgThrGlnArgProIleSerVal 340
Db 961 TACTGTCTGTTCACAAATGCTTTCATTAACCTTACCCAGAACCGGAACCCCAATGCTG 1020
Qy 341 TrpTyrlleSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrlle 360
Db 1021 TGGTACGACTTTCCTTGGCTGCTGCAATGCTTCAATTCCTTGTATATCCCTTCTGTAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnIleValAlaPheTrpIleIleLeuCysValThrIleTrp 380
Db 1081 CTTTGTGTACAGGCGTTTCCAGAGGCTTCTGGAAGATCTTGTGTGACAAAGCAA 1140
Qy 381 ProAlaLeuSerGlnAnGlnSerValSerSer 391
Db 1141 CCAGCGCTGTACAGAACGATCATCTTCT 1173

RESULT 2
US-10-626-445-6
; Sequence 6, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Idu, Changlu
; TITLE OR INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-445-6

Alignment Scores:
Pred. No.: 8.99e-183 Length: 1176
Score: 1745.00 Matches: 332
Percent Similarity: 89.26% Conservative: 17
Best Local Similarity: 84.91% Mismatches: 42
Query Match: 85.21% Indels: 0
DB: 18 Gaps: 0

US-10-626-445-8 (1-391) x US-10-626-445-6 (1-1176)
Qy 1 MetSerGluSerAnSerThrGlyIleLeuProProAlaIleValProLeuAlaPhe 20
Db 1 ATGTGGAGCTTAACATGCTGATCTTGGCCACCTGCTGAGCTCCCTTGCACTTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTAATGCTTCATTGGCTTGGCTATATGATGATGATGATGATGATGATGATGATGAT 120
Qy 41 ValValAspArgAnSerThrGlyIleLeuProProAlaIleValProLeuAlaPhe 60
Db 121 GTGGTGGACGAAACCTTACACATGAAATATATATATATATATATATATATATATAT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrlleProHisValleuPheAnTrp 80
Db 181 GACTCTCTGCGGTGATTTGATTCATTCCTGACATCCCTGACGCTGTTTAACTGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrlleLeuLeuCythrAla 100
Db 241 AATTTTGAAGTGAATCTGCATGTTTGGCTCATCTACTGATCTTTTGTGACCGCA 300

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Oy      101 SerValAlTyAsnIleValLeuIleSerTyAspArgTrpGlnSerAlaSerAlaVal 120
Db      301 TCGGTTACAGAAATGTTCTCATTAAGTACAGATCGAATACAGACAGTTCACAAAGCGCTGG 360
Oy      121 SerTyAspAlaGlnIleThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140
Db      361 CGTTATAGAGCACAGCACACTGGCACTCGAAATATGTTGCTCATTAATGGTGGCTTTGG 420
Oy      141 IleLeuAlaPheLeuValIleGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db      421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTCTTGSAAGACAGC 480
Oy      161 ThrAsnThrLysAspGlyLupProGlyPheValThrGlyTrpValIleLeuThrIleThr 180
Db      481 ACCAACACACAGAGAGCGAGCGCTGGCTTTGTTACTGAGGTGATCACTCCGCCATTAA 540
Oy      181 MetLeuLeuGlnPheLeuLeuProValIleSerValAlaTyPheAsnValGlnIleTy 200
Db      541 GCATTCTTGGAATTCCTGCTCCCTGCTCTCTGCTCTGCTGCTATTTCATGTTACGATTAC 600
Oy      201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerIleAlaGlyPheSerThr 220
Db      601 TGGACCTCTGGAGAGCGTGGAGTCTCAATAGGTGCTTACGCCACCGCTGATTCATCGCT 660
Oy      221 ThrSerSerSerAlaSerGlyIleMetIleValGlnAlaGlyValAlaCysArgThrSerAsn 240
Db      661 ACCCTTTCCAGGGGCGACCTGAGACCTCACACAGAACTGGGTGGCTGTGTGGACAACTCT 720
Oy      241 ProGlyLeuLysGlnSerAlaIleAspArgHisSerGlnSerProArgArgLysSerSer 260
Db      721 CCTGAATTAAAGAAACCAAGCCGATCTCTTCATTCCAAAGATCCACAGAGAAAGACCT 780
Oy      261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db      781 CTCCTGGTGTCTCTTAAGACCTCAACAGAGCGGATCATGTGCTTCAAAATGGGCTTCC 840
Oy      281 PheTrpArgSerGlnSerAlaIleLeuArgGlnArgGlnTyrlAlaGluLeuLysGly 300
Db      841 TTCTCCCGATTCAGAAAGCCAGTGTCTTCCAGAGAGACACGTGAGCTTCTTCAGAGCGC 900
Oy      301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db      901 AGGAAGCTAAGCAAGTCCGTAAGTGTCTCTCGAAGTCTTTGGCAATTTGCTGGGCTCCG 960
Oy      321 TyrCysLeuPheThrIleValLeuSerThrTyrlProArgThrGlnArgProLysSerVal 340
Db      961 TATTCCCTGTTCAACAATGTTCTTTTCAACTTATCCGAGAGGGGAGGCGCCCAATCGATT 1020
Oy      341 TrpTyrlSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTy 360
Db      1021 TGGTACACATAGCCCTTTTGGCTTACAGTGGTCAATTCACTATTAATATCCCTTTCTAT 1080
Oy      361 ProLeuCysHisArgArgPheGlnTyrlAlaPheTrpLysIleLeuCysValThrIysTrp 380
Db      1081 CCTTTGTGCACAGACGTTTCCAGAAAGCTTTCTGGAAAGATCTCTGTGTGACAAAGCA 1140
Oy      381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391
Db      1141 CCAGACCTTCCACAGACCACAGTCAATTTCT 1173

RESULT 3
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monema, Frederick J. Jr.
; APPLICANT: Moore, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor

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FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-09-812-216-1

Alignment Scores:
Pred. No.: 2,92e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.32% Conservative: 40
Best Local Similarity: 68.11% Mismatches: 82
Query Match: 66.92% Indels: 3
DB: 9 Gaps: 2

US-10-626-445-8 (1-391) x US-09-812-216-1 (1-1173)

QY 1 MetSerGIuSerAAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
D 1 ATGCCAGATCTAAATAGACCAATCAATTTATCATAGACCTCGGTACTTATGACATTT 60
QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIleLeuAlaPhe 40
D 61 TTTATGTCCTTATGTAAGCTTTTCCTATATATGCTAAGAAAGCTTTGGTCAATTAAGCTTT 120
QY 41 ValValaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
D 121 GGGGTGGACAAAAACCTTAGACATGAGATGATTTATTTTCTTAACCTGGCCATCTCT 180
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
D 181 GACTTCCTTGGGGGTGATCTCCATTCCTTGTGATCATCCCTCACACGCTGTTCGAATGG 240
QY 81 AsnPheGlySerGlyIleCysMetPheThrPheLeuIleThrAspTyrLeuLeuCysThrAla 100
D 241 GATTTTGGAAAGAAATCTGTGATATTTTGGCTCACACTGACTATCTGTTATGTACAGCA 300
QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
D 301 TCTGTATATTAACATTTGCTCCTCATCAAGCATATGATCATCTGTCACTCAATATGCGTG 360
QY 121 SerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTyr 140
D 361 TCTTATTAAGACCAACATATCTGGGCTCTTGAAGATTTGATCTGATGGTGGCCGTTTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerThrPheAsnSer 160
D 421 GTGGCGCTCTTATGTAATGGCCAAATGATTTCAAGTTCAGAGCTTGGAAAGGAA 480
QY 161 ThrAsnThrLysAspCysGlyProGlyPheValIleThrGluTyrTyrIleLeuThrIleThr 180
D 481 GGTAAGT-----GATGTGAACCTGATTTTTCGGAAATGATCAATCTTCGCAATCAC 534
QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
D 535 TCATTCCTTGAATTCGTATCCCAATCACTTATGTCGCTTATTTCAACATGAAATATTAT 594
QY 201 ThrPheLeuThrPheValArgAlaIleLeuSerArgCysProSerHisAlaGlyPheSerThr 220
D 595 TGGAGCCCTGTGAAGCGTATCATCTCAATGAGTGCACAAAGCCATCTGAGTCACTGCT 654
QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
D 655 GTCTCTTCCACATCTGTGGACATCTCAATTCAGAGGTAGACATCTTCAAGAGATCTCTT 714
QY 241 ProGlyLeuLysGluSerAlaAlaSerArgHisArgSerGluSerProArgArgLysSerSer 260

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Db 715 TCTGATCGACAGAGTTCTCGATCTTTCATTGACAGACAGAGAGAGAGTAGT 774  
Qy 261 ILeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheIysValGlySer 280  
Db 775 CTCATGTTTCTTCACAGACCAAGATGATGCAATGCAATGCTTCCAAAATGGGTTCC 834  
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTrpAlaGluLeuLeuArgGly 300  
Db 835 TTCTCCCAATCATGATCTTGAGCTTTCACCAAAAGGAGAACATGTTGAATCGCTTAGAGCC 894  
Qy 301 ArgIysLeuAlaArgSerLeuAlaAlaLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
Db 895 AGGAGATTAGCCACAGTCACTGGCCATTCTCTAGGGGTTTGTGTCTGGGCTCCA 954  
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProIysSerVal 340  
Db 955 TATTCTCTGTTCCAAATTCCTTTCATTATTTCTCCACACAGAGTCTTAATTCAGTT 1014  
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360  
Db 1015 TGGTATAGAAATTCATTTGGCTTCAGTGGTTCAATTCCTTGTCAATCTCTTTGTAT 1074  
Qy 361 ProLeuCysHisArgArgPheGlnIysAlaPheTrpIysIleLeuCysValThrIysTrp 380  
Db 1075 CCATTGTGTCAACAGCGCTTTCAAAAGGCTTTCTTGAAAATATTGTTATAAAAAGCAA 1134  
Qy 381 ProAlaLeuSerGln--AangIserValSerSer 391  
Db 1135 CCTTACCATCAACACACAGTGGGTCAATCTTCT 1170

## RESULT 4

US-09-910-411-1  
; Sequence 1, Application US/09910411  
; Patent No. US20020137054A1  
; GENERAL INFORMATION:  
; APPLICANT: Bergsma, Derk  
; APPLICANT: Fitzgerald, Laura  
; APPLICANT: Li, Xiaolong  
; APPLICANT: Michalovich, David  
; APPLICANT: Zhu, Yuan  
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor  
; FILE REFERENCE: GP70655-2C1  
; CURRENT APPLICATION NUMBER: US/09/910,411  
; PRIOR FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: 09/693,761  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/497,790  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/431,898  
; NUMBER OF SEQ. ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ. ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-910-411-1

## Alignment Scores:

Pred. No.: 2,92e-141 Length: 1173  
Score: 1370.50 Matches: 267  
Percent Similarity: 78.32% Conservative: 40  
Best Local Similarity: 68.11% Mismatches: 82  
Query Match: 66.92% Indels: 3  
Gaps: 2

US-10-626-445-8 (1-391) x US-09-910-411-1 (1-1173)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20  
Db 1 ATGCCAGATGACTATGACACATCAATTTATTCACCTAGACACTGCTGTACTTATGACATTT 60  
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40

Db 61 TTTATGCTCTTACTACTTTTGGCTATATATGCTGGAAATGCTTGGTCAATTTAGCTTTT 120  
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 121 GTGGTGACAAAACCTTATACATCGAAGTATATTTTCTTAACTTGGCCACTCTT 180  
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80  
Db 181 GACTTCTTGTGGGTGATCTTCATTCCTTTGTATATCCCTCACAAGCGTGTTCGATGG 240  
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleLeuCysThrAla 100  
Db 241 GATTTGGAAAGGAAATCTGTATATTTGGCTCACACATGACATATCTGTATATACAGCA 300  
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
Db 301 TCTGATATATACATTTGCTCATACATGATGATGATGATGATGATGATGATGATGATG 360  
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIysIleValAlaGlnMetValAlaValTrp 140  
Db 361 TCTTATAGAACTCAACATACCTGGGCTTGAATTTGTTACTGTGATGGTGGCGTTGG 420  
Qy 141 ILeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIysAsnSer 160  
Db 421 GTCTGGCCCTTCTTATGAAATGGCCAAATGATCTGTATGACAGTCTTGGAAAGATGA 480  
Qy 161 ThrAsnThrIysAsnGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180  
Db 481 GGTAATG----GAAATGAACTGGATATTTTTCGAAATGTACATCTTCCCATCA 534  
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
Db 535 TCATTTGGAAATTCGATATCCAGTCACTTATGTGCTTATTTCAACATGAATATTTAT 594  
Qy 201 TrpSerLeuTrpIysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
Db 595 TGGAGCCTGTGGAAAGGTGATCATCTCAGATGGTGCAAAAGCATCTGGACTGACTGCT 654  
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
Db 655 GTCTCTTCCAAACATCTGTGGACCTCATTCACAGGTAGACTATCTTCAGAGATCTCTT 714  
Qy 241 ProGlyLeuIysGluSerAlaAlaSerArgHisSerGluSerProArgArgIysSerSer 260  
Db 715 TCTGATCGACAGAAATGCTCGATCTTTCATTGACAGAGACAGAGAGAGAGTAGT 774  
Qy 261 ILeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheIysValGlySer 280  
Db 775 CTCATGTTTCTTCACAGACCAAGATGATGCAATGCAATGCTTCCAAAATGGGTTCC 834  
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTrpAlaGluLeuLeuArgGly 300  
Db 835 TTCTCCCAATCATGATCTTGAGCTTTCACCAAAAGGAGAACATGTTGAATCGCTTAGAGCC 894  
Qy 301 ArgIysLeuAlaArgSerLeuAlaAlaLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
Db 895 AGGAGATTAGCCACAGTCACTGGCCATTCTCTAGGGGTTTGTGTCTGGGCTCCA 954  
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProIysSerVal 340  
Db 955 TATTCTCTGTTCCAAATTCCTTTCATTATTTCTCCACACAGAGTCTTAATTCAGTT 1014  
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360  
Db 1015 TGGTATAGAAATTCATTTGGCTTCAGTGGTTCAATTCCTTGTCAATCTCTTTGTAT 1074  
Qy 361 ProLeuCysHisArgArgPheGlnIysAlaPheTrpIysIleLeuCysValThrIysTrp 380  
Db 1075 CCATTGTGTCAACAGCGCTTTCAAAAGGCTTTCTTGAAAATATTGTTATAAAAAGCAA 1134  
Qy 381 ProAlaLeuSerGln--AangIserValSerSer 391



Qy 361 ProLeuCyshisArgArgPheGlnIleValAlaPheTrpIleLeuCyValAlaThrIleTrp 380  
Db 1075 CCAATTGGTGCACAAAGCGCTTTTCAAAAAGCTTTCTTGAATAATTTTGTATPAAAAAGCAA 1134  
Qy 381 ProAlaLeuSerGln--AasnGlnSerValSerSer 391  
Db 1135 CCTTACATCATCAACACAGCTCGGTCAGTATCTTCT 1170

RESULT 6  
US-09-876-252-13  
Sequence 13, Application US/09876252  
Publication No. US20030018182A1  
GENERAL INFORMATION:  
APPLICANT: Behan, Dominic P.  
APPLICANT: Lehmann-Brunsmma, Karin  
APPLICANT: Chalmers, Derek T.  
APPLICANT: Lowitz, Kevin P.  
APPLICANT: Lin, I-Lin  
APPLICANT: Dang, Huong T.  
APPLICANT: Chen, Ruoping  
APPLICANT: Law, Chen W.  
TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Rec  
FILE REFERENCE: ASEN-0054  
CURRENT APPLICATION NUMBER: US/09/876,252  
CURRENT FILING DATE: 2001-06-07  
PRIOR APPLICATION NUMBER: 09/416,760  
PRIOR FILING DATE: 1999-10-12  
PRIOR APPLICATION NUMBER: 09/170,496  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: 60/110,060  
PRIOR FILING DATE: 1998-11-27  
PRIOR APPLICATION NUMBER: 60/120,416  
PRIOR FILING DATE: 1999-02-16  
PRIOR APPLICATION NUMBER: 60/121,852  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/109,213  
PRIOR FILING DATE: 1998-11-20  
PRIOR APPLICATION NUMBER: 60/123,944  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,945  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,948  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,951  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,946  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123,949  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/152,524  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: 60/151,114  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: 60/108,029  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: 60/136,436  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,439  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/136,567  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/137,127  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/137,131  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/141,448  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: 60/136,437  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/156,555  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,634

PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/156,653  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 60/157,280  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,294  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,281  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/157,282  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/156,633  
PRIOR FILING DATE: 1999-09-29  
NUMBER OF SEQ ID NOS: 146  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 13  
LENGTH: 1173  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-876-252-13

Alignment Scores:  
Pred. No.: 2,92e-141 Length: 1173  
Score: 1370.50 Matches: 267  
Percent Similarity: 78.32% Conservative: 40  
Best Local Similarity: 68.11% Mismatches: 82  
Query Match: 66.92% Indels: 3  
DB: 10 Gaps: 2

US-10-626-445-8 (1-391) x US-09-876-252-13 (1-1173)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20  
Db 1 ATCCAGATATCTAATGACCAATCAATTTATCTAGCAGCTGTTACTTACGATTT 60  
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIleLeuAlaPhe 40  
Db 61 TTTATGTCCTTACTTACTTCTTTGCTATATGCTAGAAAGCTTGTCTTTAGCTTTT 120  
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 121 GTGTGACAAAGAACTTACATGACATGAGTAGTATTTTCTTAACTTGGCCATCTT 180  
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIleuPheAsnTrp 80  
Db 181 GACTCTTTGTGGGTGATCTCATCTCTTTGTATCATCCCTCACAGCGTGTGATGG 240  
Qy 81 AsnPheGlySerGlyIleCyshMetPheTrpLeuIleThrAspTyrIleLeuLeuCyThrAla 100  
Db 241 GATTTTGAAAGAAATCTGTATATTGGCTCCTACCTGACCTATCTGTATGTACAGCA 300  
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
Db 301 TCTGTATATPACATGTGCTCATCATGATGATGATGATGATGATGATGATGATGATG 360  
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetValIleValAlaGlnMetValAlaValTrp 140  
Db 361 TCTTATAGAACTGAACATACCTGCTGCTGAATGTTACTGATGATGATGATGATGATG 420  
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160  
Db 421 GTCTGCGCTTCTTGAATGAGTGGCCAAATGATCTTCTTCAAGCTTGAAGATGAA 480  
Qy 161 ThrAsnThrIleAspCyshGluProGlyIlePheValThrGluTrpTrpIleLeuThrIleThr 180  
Db 481 GGTAATG-----GAAATGTAAGCTGGAATTTTTCGAAATGTAACCTTGCATACCA 544  
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
Db 535 TCATTTCTGGAATTCGATCCAGTCACTTATAGTGGCTTATTTCAACATGATATTTAT 594  
Qy 201 TrpSerLeuTrpIleArgArgAlaLeuSerArgCyshSerHisAlaGlyPheSerThr 220

```

Db      595 TGGAGCCTGTGAGAGCGTATCATCTCAGTAGTGCCAAAGCCATCTGGACTGCT 654
Qy      221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCyArgThrSerAsn 240
Db      655 GTCTCTTCCAACTCTGTGACATCTCATTCAGAGGTAGACATATCTTCCAAAGGAGATCTCTT 714
Qy      241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGlySerProArgArgLysSerSer 260
Db      715 TCTGCATGCACAGAACTTCTGCATCTTTCATTCAGAGAGACAGAGAGAAAGAGTACT 774
Qy      261 IleLeuValSerLeuArgThrHisIleMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db      775 CTCATGTTTCTTCCAAAGAACCAAGATGATAGCAATACATTCCTTCCAAATAGGGTCTCC 834
Qy      281 PheTPArgSerGluSerAlaAlaLeuArgGlnArgGlnIleThrAlaGluLeuLeuArgGly 300
Db      835 TTCTCCCAATCAGATTCGTAGCTCTTCCACCAAGGAAACATGTTAACTGCTTAGAGCC 894
Qy      301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db      895 AGGAGATTAGCCACAGTCACATGCGCATTCCTTAGGGGTTTTCCTGTGCTGGCTGCCA 954
Qy      321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db      955 TATTCCTGTTCACATTCCTCTTTCATTTATTCCTCAGCAACAGTCTTAATCAGTT 1014
Qy      341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db      1015 TGGTATAGAAATGCAATTTGGCTTCAGTGATTCATTCCTTTGTCATCTCTTTGTAT 1074
Qy      361 ProLeuCysHisArgArgPheGlnLysValAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db      1075 CCATTGTGTCAACAGGCTTTCAAAGGCTTTCTTGAATAATTTTGTATATAAAGCA 1134
Qy      381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db      1135 CCTCTACATCAACACAGTCGCGTCAGTATCTTCT 1170

RESULT 7
US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-193-1

Alignment Scores:
Pred. No.: 2,92e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.32% Conservative: 40
Best Local Similarity: 68.11% Mismatches: 82
Query Match: 66.92% Indels: 3
DB: 13 Gaps: 2

US-10-626-445-8 (1-391) x US-10-052-193-1 (1-1173)
Qy      1 MetSerGluSerAsnSerThrGlyIleLeuProPheAlaAlaGlnValProLeuAlaPhe 20
Db      1 ATGCCAGATCACTAAATAGCAATTCATTCATCTAGACATCTAGACATCTTACCATTT 60
Qy      21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIleLeuAlaPhe 40

```

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Db      61 TTTATGCTCTTAGTAGCTTTTCTGTATTAATGCTAGAGAAATGCTTGGTCAATTTAGCTTTT 120
Qy      41 ValIleAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db      121 GTGGTGGACCAAAACCTTAGACATGAAAGTATTTTTTTTCTTAATCTGGCCATCTCT 180
Qy      61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
Db      181 GACTTCTTTGGTGGTGTATCTCAATCTCTTGTACATCTCCACACAGCTGTTCGAATGG 240
Qy      81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db      241 GATTTTGGAAAGGAATCTGTATTTTGGCTACTAGTACTAGTATCTGTATGACAGCA 300
Qy      101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db      301 TCTGTATATTAACATTTGCTCTCATGTAGATCATACCTGTACGTCTCAATGCTGTG 360
Qy      121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140
Db      361 TCTTATAGAACTCAACATACGAGGCTTGAAGATTTGTAATCTGAATGGTGGCCGTGG 420
Qy      141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db      421 GTCGTGGCTTCTTATGTAATGGCCATGATTCATGATTCAGAGTCTTGGAAAGATGAA 480
Qy      161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
Db      481 GGTAGT-----GAATGTGAACCTGATTTTTCGAATGGTATCATCTCTCCATCAACA 534
Qy      181 MetLeuLeuGlnPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db      535 TCATCTTGGAAATTTGTATCCAGTCATCTTAGTGGCTTATTTTGAACATGAATATTTAT 594
Qy      201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db      595 TGGAGCCTGTGAGAGCGTATCATCTCAGTAGTGCCAAAGCATCTCGAGCTAGCTGT 654
Qy      221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db      655 GTCTCTTCCAACTGTGTGACATCTTCATTCAGAGGTAGACATATCTTCCAAAGGAGATCTCT 714
Qy      241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db      715 TCTGCATGCACAGAACTTCTGCATCTTTCATTCAGAGAGACAGAGAGAAAGAGTACT 774
Qy      261 IleLeuValSerLeuArgThrHisIleMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db      775 CTCATGTTTCTTCCAAAGAACCAAGATGATAGCAATACATTCCTTCCAAATAGGGTCTCC 834
Qy      281 PheTPArgSerGluSerAlaAlaLeuArgGlnArgGlnIleThrAlaGluLeuLeuArgGly 300
Db      835 TTCTCCCAATCAGATTCGTAGCTCTTTCACCAAGGAAACATGTTGAATGCTTAGAGCC 894
Qy      301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db      895 AGGAGATTAGCCACAGTCACATGCGCATTCCTTAGGGGTTTTCCTGTGCTGGCTGCCA 954
Qy      321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db      955 TATTCCTGTTCACATTCCTCTTTCATTTATTCCTCAGCAACAGTCTTAATCAGTT 1014
Qy      341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db      1015 TGGTATAGAAATGCAATTTGGCTTCAGTGATTCATTCCTTTGTCATCTCTTTGTAT 1074
Qy      361 ProLeuCysHisArgArgPheGlnLysValAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db      1075 CCATTGTGTCAACAGGCTTTCAAAGGCTTTTGAATAATTTTGTATATAAAGCA 1134
Qy      381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391

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[illegible]

QY	101	SeRvAlTYrAnIlIeValLeuIlIeSeRvTYrApAaRgYrGInSeRvAlSeRAnIlAlaVAl	120
Db	301	TCTGATATTAACATTTGCTCTCAAGACTATAGTCAATACCTGCTCAAGTCTCAATATGCTG	360
QY	121	SeTYrArGAlaGInHleThrGlyIlIeWeThySlIeValAlaGInMeTValAlaValATp	140
Db	361	TCTTATATAGACATCAACATACCTGGGGTCTTGAAGATTGTTAAGTCTGATGATGATGGCCGTTTGG	420
QY	141	IlIeUeUAlaPheLeUValaAsnGlyPProMeTIlIeUeUAlaSerAaPSeRTpIyVaSnSeR	160
Db	421	GTGCTGGGCTTCTTGAATATGGGCCAAATGATATTCATAGTTTCAAGACTCTTGGAAAGATGA	480
QY	161	ThraSeNTrIlyAaPcYsGluPProGlyPheValThrIuTTPYrIlIeUeThrIlIeThr	180
Db	481	GGTAGT-----GAATGTGAACCTGGATTTTTCGGAAATGTACATCTCTTGCCATCA	534
QY	181	MeTleUeUgluPheLeUeUProValIlIeSeRValaATyRpheAaSVaGInIleTYr	200
Db	535	TCATTTCTTGAATTCGTGATCCAGTACCTTAAGTCGCTTAATTTTCAACATGAATATTTAT	594
QY	201	TPSeRTleUTpIyVaRArGAlaLeUSeRrYrGcYpProSeRHIleAlGlyPheSeRThr	220
Db	595	TGGAGCCCTGTAAGCCGTGATCATCTCACTGATGTCGCAAAACCACTTGGACCTGACTCT	654
QY	221	ThreSeRSeRAlaSeRGIyHIleUeUHIaRgaIlAglyValaIaCyArGThSeRAn	240
Db	655	GTCTCTTCCAAACATCTGTGACACCTCATTCAGAGTAACTATCTTCAAGAGATCTCT	714
QY	241	ProGlyLeUlybGluSeRAlaIaSeRrghISeRGIuSeRProArGArGlySeRSeR	260
Db	715	TCTGCATCGAAGAACTTCGTCATCTCTTATTCAGAGACAGACAGAGAAAGATAGT	774
QY	261	IlIeUeUAlaSeRleUArghThHleMeTaaNSeRSeRIlIeThraIaPheIyValGIySeR	280
Db	775	CTCAATGTTTCTCAAGAACCAAGATGAATAGCATACATACATTCGTTCCAAATGGGTTCC	834
QY	281	PheTArGSeRGIuSeRAlaIaLeUeUArGInArGluTyralAGluLeUeUArGly	300
Db	835	TTTCCCAACATCAGATTCTGTAGCTCTTCAACAAAGGAAACATGTGAACCTGTTAGACCC	894
QY	301	ArGlyleUAlaArGSeRleUAlaIlIeUeUSeRAlaPheAlaIleCySTpAlaPro	320
Db	895	AGGAGATTAGCCAAGTCACTGCGCATTCCTTAAAGGGATTYYYTGCTGTGCTGGGCTCCA	954
QY	321	TyrCysleUPheTrIlIeValIeUSeRThrTYrProArGThnGluArGProIySeRSeRAl	340
Db	955	TATTCCTCTGTTCAACATTCCTTTTCATTTATTTCTCAGCAACAGGCTCTTAATCAAGTT	1014
QY	341	TrpTYrSeRlIeAlaPheTrpLeUGInTrpPheAnSeRpheValaSnProPheLeUTyr	360
Db	1015	TGGATATAGAAATGGCATTTTGGCTTCAGGGTTCAATTCCTTTGTCAATCCTTTTGTAT	1074
QY	361	ProleUcYvHIlaRgArGpHeGInIyAlaPheTrpIySlIeUeCYeValThrIySTp	380
Db	1075	CCATTGTGTCAAAAGCCCTTCAAAAGCCCTTCTGAAAATAATTTGTATMAAAAGCAA	1134
QY	381	ProAlaIeUSeRGIu---AsnGInSeRValSeRSeR	391
Db	1135	CCTTACATCAACAACAGTGGGTCAATATCTTCT	1170
<p>RESULT 9</p> <p>US-10-354-769-1</p> <p>Sequence 1, Application US/10354769</p> <p>Publication No. US20030149242A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Pfizer Inc.</p> <p>APPLICANT: O'Reilly, Mark A.</p> <p>APPLICANT: Peter, Beate</p> <p>TITLE OF INVENTION: NOVEL POLYPEPTIDE</p> <p>FILE REFERENCE: PCI0373B</p> <p>CURRENT APPLICATION NUMBER: US/10/354,769</p> <p>CURRENT FILING DATE: 2003-01-30</p>			



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; PRIOR APPLICATION NUMBER: US 09/598,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-769-1

Alignment Scores:
Pred. No.: 2,92e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.32% Conservative: 40
Best Local Similarity: 68.11% Mismatches: 82
Query Match: 66.92% Indels: 3
DB: 15 Gaps: 2

US-10-626-445-8 (1-391) x US-10-354-769-1 (1-1173)
QY 1 MetSerGluSerAsnSerThrGlyLeuProProAlaAlaGlnValProLeuAlaPhe 20
DB 1 ATGCCAGATCACTAATAGCAACAATTCATTCATCAAGACATCGTGAATCTTACATTT 60
QY 21 LeuMetSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIleLeuAlaPhe 40
DB 61 TTTATGCTCTTATGATCTTTCTCTATATGCTAGAAATGCTTTGGTCACTTTAGCTTTT 120
QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB 121 GTGGTGAGCAAAACCTTAGCATGAGATGATATTTTCTTAATCTTGCCATCTCT 180
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
DB 181 GACTTCCTTGTGGTGATCTCCATTCCTTGTGATCCCTCCACACGCTGTTGCAATGG 240
QY 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
DB 241 GATTTTGAAAGAAATCTGTATTTTGGCTCACTGACTATCTGTTATGTCAGCA 300
QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB 301 TCTGATATTAACATTTGCTCTCATCGATGATGATCCATGCTGCTCAAAATGCTGG 360
QY 121 SerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMetValAlaValTrp 140
DB 361 TCTTATTAACAACCACTACTGCGGTCTTGAAGATGTTACTCTGATGCTGCCCTTTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160
DB 421 GGGCGGCTCTTATGATGATGGCCAAATGATTTCAAGCTTCAAGCTTGAAGATGAA 480
QY 161 ThrAsnThrIleAspCysGluProGlyPheValIleThrGluTrpTyrIleLeuThrIleThr 180
DB 481 GGTACT-----GAATGTGAACCTGGAATTTTGGGAATGTATCATCTTCCATCA 534
QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
DB 535 TCATCTCTTGGAATTCGTATCCAGTCATCTTAGTCGCTTATTTCAACATGAAATTTTAT 594
QY 201 TrpSerLeuTrpIleArgAlaGlnLeuSerArgCysProSerHisAlaGlyPheSerThr 220
DB 595 TGGACCTCTTGGAAGCGATCATCTCACTAGTGCCAAAGCACTCTGGACTGCTGCT 654
QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
DB 655 GCTCTCTTCAACATCTGTGGAACATCTCATGAGGTAAGCTATCTTCAAGAGATCTCTT 714
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QY 241 ProGlyLeuValGluSerAlaAlaSerArgHisSerGluSerProArgArgIleSerSer 260
DB 715 TCTGCATGACACAGAACTTCTGCATCTTTCACTTAGAGAGACAGAGGAAAGATGACT 774
QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheValAlaGlySer 280
DB 775 CTCATGCTTTCTCAAGAACCAAGATGAAATGCAATATGCTTCCAAATAGGCTTCC 834
QY 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgIleTyrAlaGlnLeuLeuArgGly 300
DB 835 TTCTCCCAATCAGATTCGTAGCTTCTTCCAAAGGGAACAGTGAACGTGTAAGACC 894
QY 301 ArgValLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
DB 895 AGAGATTAAGCCAGTCACTGCGCATTCCTTCAAGGCGTTTGGCTGTGCTGGCTCA 954
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProIleSerVal 340
DB 955 TATTCCTGTTCCAGAAATGCTCTTTCACTTATTCCTCAGAACAGTCCATAATCAGTT 1014
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
DB 1015 TGGTATGAATATGATTTTGGCTTCAAGTTCATTCCTTGTCAATCTCTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnIleValAlaPheTrpIleLeuCysValThrIleTrp 380
DB 1075 CCATTGTGTCAAGCGCTTCAAAAGGCTTTCTGAAAAATTTTGTATTAATAAAGCA 1134
QY 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
DB 1135 CCTCACCATCAACAACAGTCGTCAGTATCTTCT 1170

RESULT 10
US-10-393-807-13
; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chem, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: APO0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-393-807-13

## Alignment Scores:

Pred. No.:	2,92e-141	Length:	1173
Score:	1370.50	Matches:	267
Percent Similarity:	78.32%	Conservative:	40
Best Local Similarity:	68.11%	Mismatches:	82
Query Match:	66.92%	Indels:	3
		Gaps:	2

US-10-626-445-8 (1-391) x US-10-393-807-13 (1-1173)

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QY 1 MetSerGlnSerAnSerThrGlyLeuProValAlaGlnValProLeuAlaPhe 20
DB 1 ATCCGATACATACATACATACATACATACATACATACATACATACATACAT 60
QY 21 LeuMetSerPheAlaPheAlaIleMetValGlyValAlaValIleLeuAlaPhe 40
DB 61 TTATATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTT 120
QY 41 ValValAspArgAnSerThrGlyLeuSerAnSerPhePheLeuAnSerValIleSer 60
DB 121 GTGGTGACAAAACCTTACATCAGAGTAGTATTTTCTTACCTGGCCATCTCT 180
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAnSer 80
DB 181 GACTCTTTGTGGGTGATCTCATCTTTGTACATCCCTCACACGCTGTTGAAATGG 240
QY 81 AsnPheGlySerGlyIleCysMetPheTyrPheIleThrAspTyrLeuLeuGlyThrAla 100
DB 241 GATTTTGGAAGAAACCTGTGATTTTGGCTCATCTACATCATCTGTTATGTACGCA 300
QY 101 SerValTyrAnSerIleValIleSerTyrAspArgTyrGlnSerValSerAnAlaVal 120
DB 301 TCTGTATATACATGCTGCTCATCAGTATGATGATGATGATGATGATGATGATG 360
QY 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
DB 361 TCTTATGAGACTCAACATCTAGGCGCTTGAAGATGTTACTGATGATGATGATG 420
QY 141 IleLeuAlaPheLeuValIleGlyProMetIleLeuAlaSerAspSerTyrPheAnSer 160
DB 421 GTCTGTGCTTCTTATGAGATGAGGATGATGATGATGATGATGATGATGATG 480
QY 161 ThrAsnThrLysAspCysGlnProGlyPheValThrGlnTyrPheIleThrIleThr 180
DB 481 GGATAGT-----GATGTGAACCTGGATTTTTCGAAATGATGATGATGATG 534
QY 181 MetLeuLeuGlnPheLeuLeuProValIleSerValAlaTyrPheAnValGlnIleTyr 200
DB 535 TCATTTCTTGGAAATCGGATCCGATCCGATCATCTTATGCTTATTCACATGAAATATTAT 594
QY 201 TTPSerLeuTyrPheValGlyAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
DB 595 TGAGGCTGTGAGAGCGGTGATCATCTCAGAGGCGCAAAAGCCATCTGACCTGACGCT 654
QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAn 240
DB 655 GTCTCTTCCAACTCTGTGACACTCATTCAGAGGTAGATCATCTTCAAGAGATCTCTT 714
QY 241 ProGlyLeuValGlnSerAlaAlaSerArgHisSerGlnSerProArgArgLysSerSer 260
DB 715 TCTGCATTCAGACAGAGTTCTCGATCTTTCATTCATTCAGACAGACAGAGAGAGTAGT 774
QY 261 IleLeuValSerLeuValGlyThrHisMetAnSerSerIleThrAlaPheLysValGlySer 280
DB 775 CTATATGTTTCTTCACAGAACCAAGATGATGATGATGATGATGATGATGATG 834
QY 281 PheTyrArgSerGlnSerAlaAlaLeuArgGlnArgGlnTyrAlaGlnLeuLeuArgGly 300
DB 835 TTCTCCCAATCAAGATTTGTAGCTCTTACCAAAAGGAGGATGTTGAACTGCTTACGCC 894
QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrPalaPro 320

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DB 895 AGGAGATTAGCCAAAGCTACGCGCATCTTATGAGGCTTTTGTCTGTGGGCTCCA 954
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGlnArgProLysSerVal 340
DB 955 TATTTCTGTGTCACAAATGTGCTTATTTATTTCTCTCAGCAACAGGTCTTAATCAGTT 1014
QY 341 TTPYSerIleAlaPheTyrPheGlnTyrPheAnSerPheValAnProPheLeuTyr 360
DB 1015 TGGTATAGAAATTCATTTTGGCTTCAAGTGGTTCATTTCTTGTCAATCCTTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnLysValAlaPheTyrLysIleLeuCysValThrLysTyr 380
DB 1075 CCATGTGTCACAGCGCTTTCAAAAGCGCTTCTTAAAATATTTGTATTAAGCAA 1134
QY 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
DB 1135 CCTTACATCACAACACAGTGGTCAATGATCTTCT 1170

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## RESULT 11

US-10-417-820A-13

Sequence 13, Application US/10417820A

Publication No. US20030229216A1

GENERAL INFORMATION:

APPLICANT: Chen, Ruoping

APPLICANT: Liaw, Chen W.

APPLICANT: Lowitz, Kevin

APPLICANT: Chalmers, Derek T.

APPLICANT: Behan, Dominic P.

TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

TITLE OF INVENTION: Receptors

FILE REFERENCE: 7.US28.CON

CURRENT APPLICATION NUMBER: US/10/417,820A

CURRENT FILING DATE: 2003-04-16

PRIOR APPLICATION NUMBER: 09/416,760

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: 60/110,060

PRIOR FILING DATE: 1998-11-27

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/121,852

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/109,213

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: 60/123,944

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,945

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,948

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,951

PRIOR FILING DATE: 1999-03-12

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 155

SOFTWARE: PatentIn version 3.2

SEQ ID NO 13

LENGTH: 1173

TYPE: DNA

ORGANISM: Homo sapiens

US-10-417-820A-13

## Alignment Scores:

Pred. No.:	2,92e-141	Length:	1173
Score:	1370.50	Matches:	267
Percent Similarity:	78.32%	Conservative:	40
Best Local Similarity:	68.11%	Mismatches:	82
Query Match:	66.92%	Indels:	3
		Gaps:	2

US-10-626-445-8 (1-391) x US-10-417-820A-13 (1-1173)

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Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
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Qy 41 ValValaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACCAAAACCTTAGACATCGAAGATTATTTTCTTAATCTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIleuPheAsnTyr 80
Db 181 GACTTCTTTGGTGCTGATCTCCATCTCTTGTACATCCCTCACAGCTGTTCCGATGG 240
Qy 81 AsnPheGlySerGlyIleCyMetPheTyrPheIleThraPyrLeuLeuCyThrAla 100
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Db 301 TCTGTATTAATACATTTCTCCATCAGCTATGATCGATACCTGCTCAATGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrglylleMetIleValIleGlnMetValAlaValIleTyr 140
Db 361 TCTTATAGAACTCAACATATGCGGCTTGAAGATTGTACTGTAGTGGCCGCTTGG 420
Qy 141 IleLeuAlaPheLeuValaGngIleProMetIleLeuAlaSerAspSerTyrIleAsnSer 160
Db 421 GTGCTGGCCCTCTTACTGATGAGGCGCAATGATCTGATTTTCAAGCTTGAAGCATGA 480
Qy 161 ThrAsnThrIleAspArgGluProGlyPheValIleThrgIleTyrIleLeuThrIleThr 180
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Qy 201 TyrSerLeuTyrIleValIleuSerArgCyProSerHisAlaGlnPheSerThr 220
Db 595 TGGAGCCTGTGAGAGGATCATCTCAGTAGGTCGCAAGCATCTCGACTGCT 654
Qy 221 ThrSerSerSerAlaSerGlyHisIleuHisArgAlaGlyValAlaCyArgThrSerAsn 240
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Qy 241 ProGlyLeuIleuSerAlaIleAspArgHisSerGluSerProArgIleuSerSer 260
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Qy 361 ProLeuCyHisArgArgPheGlnIleValaPheTyrIleLeuCyValIleThrIleTyr 380

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RESULT 12
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; Sequence 1, Application US/10349253A
; Publication No. US20040043393A1
; GENERAL INFORMATION:
; APPLICANT: Aubart, Kelly
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Graybill, Todd
; APPLICANT: Li, Xiaolong
; APPLICANT: Michalovich, David
; APPLICANT: Morrow, Dwight
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AKOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C2
; CURRENT APPLICATION NUMBER: US/10/349,253A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/910,411
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-349-253A-1

Alignment Scores:
Pred. No.: 2,92e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.32% Conservative: 40
Best Local Similarity: 68.11% Mismatches: 82
Query Match: 66.92% Indels: 3
DB: 17 Gaps: 2

US-10-626-445-8 (1-391) x US-10-349-253A-1 (1-1173)
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Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
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Db 421 GTCTGGCCCTTCTTGAAGATGGCCCAATGATTCTTACGAGTCTTGGAAAGATGAA 480
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Qy 241 ProGlyLeuPlySerIleAlaSerArgHisSerGluSerProArgTyrGlySerSer 260
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Qy 301 ArgIleLeuAlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTyrAlaPro 320
Db 895 AGGAGATTACCAAGATCACTGGCATTCTTGGGGTCTTGTGTTGCTGGGCTCCA 954
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Qy 381 ProAlaLeuSerGln--AsnGlnSerValSerSer 391
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US-10-723-955-13

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/ Sequence 13, Application US/10723955
/ Publication No. US20040110238A1
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Lin, I-Lin
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lehman-Brylinska, Karin
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Gore, Martin
/ APPLICANT: White, Carol
/ TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
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/ TITLE OF INVENTION: Receptors
/ FILE REFERENCE: 7.US29.CON
/ CURRENT APPLICATION NUMBER: US/10/723,955
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: 10/417,820
/ PRIOR FILING DATE: 2003-4-16
/ PRIOR APPLICATION NUMBER: 09/416,760
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/110,060
/ PRIOR FILING DATE: 1998-11-27
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,852
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/123,944
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,945
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,948
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR FILING DATE: 1999-03-12
/ Remaining prior application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 148
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-723-955-13
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## Alignment Scores:

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Pred. No.: 2,92e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.32% Conservative: 40
Best Local Similarity: 68.11% Mismatches: 82
Query Match: 66.92% Indels: 3
DB: 18 Gaps: 2
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US-10-626-445-8 (1-391) x US-10-723-955-13 (1-1173)

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Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaIleValIleValAlaPhe 20
Db 1 ATCCAGATCTAATGACCAATCAATTTATCTACTAGACCTGTTACTTACATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIleValAlaPhe 40
Db 61 TTTATGCTTACTTACTTCTTTGCTATATGCTAGAAATGCTTTGCTATTTAGCTTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
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Qy 81 AsnPheGlySerGlyIleCysMetPheTyrPheIleThrAspTyrLeuLeuCysThrAla 100
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Db 301 TCTGATATTAACATTTGCTCATACACTATGATCGATCTGCTGATCTCAATGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaIleValAlaValTyr 140
Db 361 TCTTATGAACTCAACATCTGGGGCTTGAAGATTTACTGTGATGGGGCGTTTGG 420
Qy 141 IleLeuAlaPheLeuValIleGlyProMetIleLeuAlaSerAspSerTyrPlyAsnSer 160
Db 421 GTCTGGCCCTTCTTGAAGATGGCCCAATGATTCTTACGAGTCTTGGAAAGATGAA 480
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Db 481 GGTAGT-----GAATGTGAAGCTGATTTTTCGGAAATGACATCTTGGCAACAA 534
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValIleThrPheAsnValGlnIleYr 200
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Db 715 TCTGATCGACAGAAAGTCTCTGATCTTCAATTCAGAGGACAGAGGAGAAAGATGCT 774
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; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-782-596-13

Alignment Scores:
Pred. No.: 2,926-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.32% Conservative: 40
Best Local Similarity: 68.11% Mismatches: 82
Query Match: 66.92% Indels: 3
DB: 18 Gaps: 2

US-10-626-445-8 (1-391) x US-10-782-596-13 (1-1173)
Qy 1 MetSerGluSerAsnSerThrGlyIleuProProAlaIleGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATCAATTAATGACATCAATTAATTAATCAATCAATCAATCAATCAATCAAT 60
Qy 21 LeuMetSerPheAlaPheAlaIleuValGlyAsnAlaValIleLeuAlaPhe 40
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Qy 41 ValValaAspAsnLeuValArgIleuSerAsnTrpPhePheAsnLeuAlaIleSer 60
Db 121 GTGCTGCAAAACCTTATGACATGATGATTTTCTTATCTTACCTGACATCTCT 180
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Qy 81 AsnPheGlySerGlyIleCyMetPheTrpLeuIleThrAspTrpLeuLeuCySerThrAla 100
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Qy 141 IleuValaPheLeuValaAsnGlyProMetIleLeuAlaSerAspSerTrpIlyAsnSer 160
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Thu Apr 7 09:08:33 2005

us-10-626-445-8.rnpb

Page 15

Search completed: April 6, 2005, 22:49:14  
Job time : 780 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 6, 2005, 19:33:37 ; Search time 4204 Seconds  
(without alignments)  
3540.231 Million cell updates/sec

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Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

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Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: gb\_hic:  
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5: gb\_eest4:  
6: gb\_eest5:  
7: gb\_eest6:  
8: gb\_ges81:  
9: gb\_ges82:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	480	23.4	721	7	CO959934 AGENCOURT
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8	404.5	19.8	1773	9	AY400782 Homo sapi
9	404	19.7	1770	9	AY400784 Mus muscu

10	404	19.7	3171	3	AK080950 Mus muscu
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22	374.5	18.3	1440	9	AY404936 Mus muscu
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25	365	17.8	1200	3	AY407501 Mus muscu
26	363.5	17.7	1072	9	AY398881 Pan trogl
27	363	17.7	643	1	AL848045 AL848045
28	360.5	17.6	1161	9	AY415607 Mus muscu
29	360.5	17.6	2578	3	AK045364 Mus muscu
30	359.5	17.6	716	7	CN423054 170004245
31	359	17.5	1401	9	AY399428 Mus muscu
32	359	17.5	4124	3	AK085653 Mus muscu
33	359	17.5	4135	3	AK079597 Mus muscu
34	355.5	17.4	499	2	BF567596 UI-R-B00-
35	355.5	17.4	1069	9	AY398882 Mus muscu
36	354	17.3	1401	9	AY399426 Homo sapi
37	353.5	17.3	1125	9	AY418220 Mus muscu
38	352.5	17.2	1173	9	AY415605 Homo sapi
39	352.5	17.2	2410	3	BC035047 Homo sapi
40	350.5	17.1	2908	3	AK082016 Mus muscu
41	346.5	16.9	1173	9	AY415606 Pan trogl
42	343.5	16.8	1134	9	AY418218 Homo sapi
43	343.5	16.8	1335	9	AY418853 Mus muscu
44	334	16.3	1269	9	AY402239 Mus muscu
45	334	16.3	3113	3	AK043668 Mus muscu

## ALIGNMENTS

RESULT 1  
BX643713  
LOCUS  
DEFINITION BX643713 839 bp mRNA linear EST 04-SEP-2003  
DKFZP781C0629 r1 781 (synonym: hicc4) Homo sapiens cDNA clone  
DKFZP781C0629\_5, mRNA sequence.

ACCESSION BX643713  
VERSION BX643713.1 GI:34478046  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
EST.

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Lauber, J., Bahr, A., Mewes, H.W., Well, B., Amlid, C., Osanger, A.,  
Fobo, G., Han, W., and Wiemann, S.

TITLE EST (Lauber, J., Bahr, A., Mewes, H.W., Well, B., Amlid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS

FEATURES  
source  
1..839  
location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"

INGOLTAEDTER Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert.  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Qigen (Hilden/Germany) within the CDNA sequencing  
consortium of the German Genome Project.  
No al sequence available.  
This clone (DKFZP781C0629) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcententrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg; GERMANY; Email: clone@rzpd.de.

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/db_xref="taxon:9606"
/clone="DKFZ781C0629"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="781 (synonym: hlc4)"
/notes="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

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## ORIGIN

## Alignment Scores:

Pred. No.:	7.08e-76	Length:	839
Score:	857.00	Matches:	170
Percent Similarity:	79.12%	Conservative:	27
Best Local Similarity:	68.27%	Mismatches:	50
Query Match:	41.85%	Indels:	3
DB:	5	Gaps:	1

US-10-626-445-8 (1-391) x BX643713 (1-839)

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Qy 1 MetSerGluSerAnSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20
Db 96 ATGCGAGATCTAATACACAAATTAATTAACAGCACTGCTTACTTACATTT 155
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
Db 156 TTATATGCTTAAAGCTTTTGGCTATATATGCTAGGAATGCTTGGTCAATTTAGCTTTT 215
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnThrPhePheLeuAsnLeuAlaIleSer 60
Db 216 GTGGTGACAAACAACTTAACAGCAAGATGATTAATTTTCTTAACCTGGCCATCTCT 275
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrlleProHisValleuPheAsnTrp 80
Db 276 GACTTCTTTGGGTGATCTCATCTCTTGGACATCCCTCAGCAGCTGTTGCATGG 335
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTrpLeuLeuGlySerAla 100
Db 336 GATTTTGGAAAGAAATCTGTATTTTGGCTCACTAGCATATCTGTATGTACAGCA 395
Qy 101 SerValTyrrAsnIleValIleuIleSerTyrrAspArgTrpGlnSerValSerAsnAlaVal 120
Db 396 TCTGTATATACATGCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATG 455
Qy 121 SerTyrrArgAlaGlnIleThrGlyIleMetLeuIleValAlaGlnMetValAlaValTrp 140
Db 456 TCTTATGAACTCAACATCTGGGCTTGAAGTTTCTTACTGTCGATGGTGGCCGTTGG 515
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLeuAsnSer 160
Db 516 GTCTGGCCCTTCTTAAGTAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAAAGATGAA 575
Qy 161 ThrAsnThrTrpAspCysGluProGlyPheValThrGluTrpTrpIleLeuThrIleThr 180
Db 576 GGTATG-----GAATGTGAACCTGGATTTTTCGAAAGTATGATCCCTTGGCCATGACA 629
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrrPheAsnValGlnIleTyrr 200
Db 630 TCAATTTGGAATTCGATGCCAGTCACTTAAGTCTTATTTCAACAGTATATTTAT 689
Qy 201 TyrSerLeuTrpLeuArgAlaLeuSerArgCysProSerHisValaGlyPheSerThr 220
Db 690 TGGAGCTGTGGAAGCCTGATCATCTCAGTAGGTGCGCAAGCCATCTCGGAGCTGACGCT 749
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaIleCysArgThrSerAsn 240
Db 750 GTCTCTTCCACATCTGT-GGACACTCATTCAGAGTAGAATCTTCAAGAGATCTCTT 808
Qy 241 ProGlyLeuLeuGluSerAlaAlaSer 249
Db 809 TCTGCATCGACAGAAATCTCTGCATCC 835

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RESULT 2  
CF147821

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LOCUS CF147821 704 bp mRNA linear EST 25-JUL-2003
DEFINITION AGENCOURT 14740195 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:6971900 5', mRNA_sequence.
ACCESSION CP147821.
VERSION CP147821.1 GI:33244089
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

REFERENCE  
AUTHORS NIH-MGC  
TITLE NIH-MGC  
JOURNAL http://mgc.nci.nih.gov/  
COMMENT Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Km10A07 Bethesda, MD 20892  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: IRB102 row: b column: 07  
High quality sequence stop: 685.

## FEATURES

## Source

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1..704
location/Qualifiers
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:6971900"
  /tissue_type="mixed"
  /lab_host="DH108"
  /clone_lib="NIH_MGC_145"
  /notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XbaI/XhoI-3',
5'-EcoRV-XbaI/XhoI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1_presv.dat
a Note: this is a NIH_MGC library."

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## ORIGIN

## Alignment Scores:

Pred. No.:	2.74e-75	Length:	704
Score:	850.00	Matches:	165
Percent Similarity:	81.70%	Conservative:	27
Best Local Similarity:	70.21%	Mismatches:	41
Query Match:	41.50%	Indels:	3
DB:	7	Gaps:	1

US-10-626-445-8 (1-391) x CF147821 (1-704)

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Qy 3 GluSerAnSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPheLeuMet 22
Db 5 GATACATTAATGCAACATCAATTAATCACTAGCACTGGTATCTTAACTTATTTTATG 64
Qy 23 SerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPheVala 42
Db 65 TCTTTAGTACCTTTTGGCTATATGCTAGGAATGCTTGGTCAATTTTGGGTG 124
Qy 43 AspArgAsnLeuArgHisArgSerAsnTyrrPhePheLeuAsnLeuAlaIleSerAspPhe 62
Db 125 GACAAACCTTAAGCATGCAAGTAGTATTTTCTTAACCTTGCACATCTGCACTTC 184
Qy 63 LeuValGlyLeuIleSerIleProLeuTyrlleProHisValleuPheAsnTrpAsnPhe 82
Db 185 TTGTGGGTGTATCTCAATCTCTTGTATCATCCCTCAGCAGCTGTTGGAATGGATTTT 244

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QY 83 GlycerGlyleCyamepetherpleuilethraapryrleuCyethralaserVal 102  
 DB 245 GGAAGGAATCTGTGATTTGGCTCACTACTGATCTTTATGACACATCTGTA 304  
 QY 103 TyraenilevalleuileserTyraaparyrginservalaserValaserTy 122  
 DB 305 TATAACATTCCTCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 364  
 QY 123 ArgalaglnihethrGlyylemetylsilevalalaglnimevalalValtrileu 142  
 DB 365 AGAAGCTCAACATCTGAGGCTTGAAGATTTGATCTGATGATGATGATGATGATGAT 424  
 QY 143 AlaphelvalaserGlyProkectileuualaseraserTyraapaserThran 162  
 DB 425 GCTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484  
 QY 163 ThrlysaerCyegluProglyPhevalThrglutrTyrlleuThrlleThmetleu 182  
 DB 485 -----GAATGGAACCTGGATTTTTCGGAATGATGATCTTGCATCATCATC 538  
 QY 183 LeuglupheleuProvalleservalalalyrPheaserValglnileTytrpser 202  
 DB 539 TTGGAAATCGATCCAGTCATCTTACGCTTATTCACATGATGATGATGATGATGAT 598  
 QY 203 LeutrylsarGargalaserSerarGysproserHialaglyPheaserThrser 222  
 DB 599 CTGGAGAGCGGATCATCTCATGAGGTGCAGAACCCATCTGAGTGAAGTCTGCTCT 658  
 QY 223 SerSerAlaserGlyHialeuThraargalaglyValalaserGarg 237  
 DB 659 TCACATCTGT-CGACATCATCTGAGGTGAGTACATCTTTCAGG 702

RESULT 3  
 CFI47822 732 bp mRNA linear EST 25-JUL-2003  
 LOCUS AGENCOURT 14740187 NIH MGC 145 Homo sapiens cDNA clone  
 DEFINITION IMAGE:6971899 5', mRNA sequence.  
 CFI47822  
 ACCESSION CFI47822.1 GI:33244090  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 732)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cga@b3-remail.nih.gov  
 Tissue Procurement: GPCR Consortium  
 cDNA Library Preparation: GPCR Consortium  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: IRB102 row: b column: 06  
 High quality sequence scop: 610.  
 Location/Qualifiers  
 1. 732  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6971899"  
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 /lab\_host="DH10B"  
 /clone\_1="NIH MGC 145"  
 /note="Vector: pcDNA3.1; Site\_1: varies by clone; Site\_2:

varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XbaI/NotI-3', 5'-EcoRV-XbaI/NotI-3', 5'-EcoRV-XbaI/NotI-3', 5'-EcoRV-XbaI/NotI-3'. For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed\_places/IRB1.presv.dat  
 A Note: this is a NIH\_MGC Library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.99e-38 Length: 732  
 Score: 482.50 Matches: 97  
 Percent Similarity: 66.15% Conservative: 30  
 Best Local Similarity: 50.52% Mismatches: 56  
 Query Match: 23.56% Indels: 9  
 DB: 7 Gaps: 3  
 US-10-626-445-8 (1-391) x CFI47822 (1-732)

QY 18 LeuAlaphelMeSerSerPheAlaphelMeValalaglnimeValalValle 37  
 DB 125 CTGGCCGCGCTCATGCGCTGCTCATGCGCGCTGCGCGCTGCGCGCTGCGCGCT 184  
 QY 38 LeuAlaphelValalaserGargalaserSerarGysproserHialaglyPheaserThrser 57  
 DB 185 CTGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 244  
 QY 58 AlalaserPheleuValalaglyleuileserleProleuTyrlleProHialeu 77  
 DB 245 GCATCTCCGATCTCTGCTGCGCGCTTGCATCCCATGATGATGATGATGATGATGAT 304  
 QY 78 Phe---AenTrpaenPheglySerGlyyleCyamepetherpleuileThraapryrleu 96  
 DB 305 ACAGCGCGCTGACCTTCGCGCGCGCTTCGCAAGCTGCTGCTGCTGCTGCTGCTGCT 364  
 QY 97 LeuCythrAlaserValalaserValalaglyleuileserTyraaparyrginserval 116  
 DB 365 CTGTGACCTCTCTGCTTCAACATGCTGCTTCAACATGCTGCTTCAACATGCTGCT 424  
 QY 117 SerAlalaserTyraargalaglnihethrGlyylemetylsilevalalaglnime 136  
 DB 425 ACCGAGCGGCTCATACCGGCGCGCGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCT 484  
 QY 137 ValalValalTrpleleuAlaphelValalaglyProkectileuualaseraser 156  
 DB 485 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 535  
 QY 157 TrpLys-----AenSerThraanThraanThraanThraanThraanThraanThraan 171  
 DB 536 TGGAGAGTACTGCTCCGCGCGCGCTCATCCCGAGGCGCATCTATGCCAGTCTTC 595  
 QY 172 ThrGlutrTyrlleleuThrlleThmetleuLeugluPheleuProvalleser 191  
 DB 596 TACAACGTGATCTTCTCATCAGGCTTCACATGAGTCTTTCAGCCCTTCTCAGC 655  
 QY 192 ValalTyraPheaserValalaglyleTytrpserleu 203  
 DB 656 GTCACTTCTTAACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 691  
 RESULT 4  
 LOCUS CO959034 721 bp mRNA linear EST 17-AUG-2004  
 DEFINITION AGENCOURT 30842625 NIH MGC 146 Homo sapiens cDNA clone  
 IMAGE:7389774 5', mRNA sequence.  
 CO959034  
 ACCESSION CO959034.1 GI:51323616  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 721)

AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Dantela S. Gerhard, Ph.D.

FEATURES	Location/Qualifiers
source	1. . 721

א. מורע: חזק כד א נחמ-  
 חזקתא:

US-10-626-445-8 (1-391) X CO959034 (1-721)

Qy	MeSeGlsuSermsnSerhrglylleuProfoalaaInvalProleuAlphe	20
	.....	
Db	ATGCCAGATCTAAATGCGACATCAATTATGACTAGACATCGGTACTTGGACATTT	81
Qy	LeuMeSeSerPheAlaPheAlaIleMeValGlyAsnAlaValIalleuAlaPhe	40
	.....	
Db	TTTATGTCCTTACTACTTTTGGCTAAATGACGAAATGCTTGGTACTTTAGCTTTT	141
Qy	ValValAspArgAsnLeuAlrghIaIargSerAsnIyrPhePheLeuAsnLeuAlIleSer	60
	.....	
Db	GTCGTGACAAACCTTAGACATCGAATAGTATTTTTTTCTTAACCTTGCGCATCTCT	201
Qy	AspPheLeuValGlyLeuIleSerIleProIeuIyrIleProIaIValLeuPheAsnTrp	80
	.....	
Db	GACCTTCTTTGTGGTGTGATCTCCATCTCTTTGTGACATCCGACACGCTGTGGAAATGG	261
Qy	AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspIyrLeuLeuCysThrAla	100
	.....	
Db	GATTTTGGAAAGAAATCTGTGATTTTGGCTCAGTACGACTAATCTGTTATGACCGCA	322
Qy	SerValIyrAsnIleValLeuIleSerIyrAspArgIyrGlnSerValSerAsnAlaVal	120
	.....	
Db	CGGTATATATAGATGTCTCCCATCAGACTATGATTAATATCCTGCAATCGAAATGCTTTG	381
Qy	SerIyrArgAlaGlnHisThrGlyIleMetIys	131

Db 382 TCTTATGGAACGCCAAAAACGGGGGGCTGAAG 414

FEATURES	Location/Qualifiers
source	1. .672

## ORIGIN

US-10-626-445-8 (1-391) x CB556920 (1-672)

Qy	18	LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle	37
Db	227	CTGGCTGGCGCTCATGCGCTGCTATGCTGGCCACAGTACTGGCGAACGGCTGGTCA	286
Qy	38	LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu	57
Db	287	CTGGCTCTGTGGCGGATTTCGAGCTCCGCAACCCAGAACAACTCTTCTGTCTCAACTC	346
Qy	58	AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIleu	77
Db	347	GCCATCTCCGACATTCCTCGTGGTGCCCTTCGCATCCCATTTGACGTAACCTTAATGTCG	406
Qy	78	Phe---AsnTyrAsnPheGlySerGlyIleCysMetPheIleuTyrAspTyrLeu	96
Db	407	ACCGGCCCTTGACCTTGCGGCCGGGCGCTTCGCACAGCTGGCGTGGTGGTGAAC	466
Qy	97	LeuCyThrAlaSerValTyrAsnIleValIleuIleSerTyrAspArgTyrGlnSerVal	116
Db	467	CTGTGGCTCTCGGTCTTCAACATCGTACTCATATGACCGATTCCTGTCACTG	526
Qy	117	SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetCysIleValAlaGlnMet	136
Db	527	ACTCGAGCTGTCTCTCAACAGGGCCACGACGAGGGGACACGACGGCGCTTCGGAAGATG	586
Qy	137	ValAlaValTyrIleLeuAlaPheLeuValAsnGlyProMetCileuAlaSerAspSer	156
Db	587	GCACGTGTGTGGGTGTGGCTTCTCTGTGTATGGCGCTGCATCTCG-----AGT	637

QY	157	TriPlys	158	
Db	638	TOGGAG	643	
RESULT 6				
LOCUS	AK081248			
DEFINITION	Mus musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone C030026C22 product:MUSCARINIC ACETYLCHOLINE RECEPTOR M1, full insert sequence.			
ACCESSION	AK081248			
VERSION	AK081248.1	GI:26349070		
KEYWORDS	HTC, CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Carninci,P. and Hayashizaki,Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol.	303,	19-44	(1999)
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res.	10	(10),	1617-1630 (2000)
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,U., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sund,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kaishiyagi,K., Fujitake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuzaki,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format			
JOURNAL	Genome Res.	10	(11),	1757-1771 (2000)
MEDLINE	20530913			
PUBMED	11076861			
REFERENCE	4			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature	409,	685-690	(2001)
MEDLINE	5			
PUBMED	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.			
REFERENCE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs			
AUTHORS	Nature	420,	563-573	(2002)
TITLE	6 (bases 1 to 3816)			
JOURNAL	Adachi,J., Aizawa,K., Akimura,T., Arawaka,T., Bono,H., Carninci,P., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Hoti,F., Imocani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Kono,H., Kouda,M., Koya,S., Kurihara,C., Matuyama,T., Miyazaki,A., Murata,M., Nakamura,Y., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohnato,N., Okazaki,Y., Saito,R., Satoh,H., Sakai,C., Sakai,K., Satazume,N., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagaki,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.			
MEDLINE	10349636			
PUBMED	11042159			
REFERENCE	2			
AUTHORS	Carninci,P. and Hayashizaki,Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol.	303,	19-44	(1999)
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res.	10	(10),	1617-1630 (2000)
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,U., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sund,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kaishiyagi,K., Fujitake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuzaki,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format			
JOURNAL	Genome Res.	10	(11),	1757-1771 (2000)
MEDLINE	20530913			
PUBMED	11076861			
REFERENCE	4			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature	409,	685-690	(2001)
MEDLINE	5			
PUBMED	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.			
REFERENCE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs			
AUTHORS	Nature	420,	563-573	(2002)
TITLE	6 (bases 1 to 3816)			
JOURNAL	Adachi,J., Aizawa,K., Akimura,T., Arawaka,T., Bono,H., Carninci,P., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Hoti,F., Im			

COMMENT  
 RIKEN Yokohama Institute; 1-7-22 Suehito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-research@riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/  
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Qy 140 TrpIleuAlaPheIleuValAsnGlyProMet-----IleIleuAlaSerAspSerTrp 157
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Qy 158 -LysAsnSerThrAsnThrLysAspCysGlnProGlyPheValThrGlnTrpTyrIle 177
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ACCESSION  CD326085
VERSION     CD326085.1  GI:31090416
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SOURCE      Xenopus laevis (African clawed frog)
ORGANISM   Xenopus laevis
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Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 853)
REFERENCE  NIH-MGC http://mgc.nci.nih.gov/.
TITLES    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: c9apbs-r@mail.nih.gov
          Tissue Procurement:
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
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 Db 616 -----TTCTGGCAATCTTGTGTGAAAGAACTGTGCGCTCGGGAGAGTCTTC 666  
 QY 170 -----PheValThrGluTrpTyrlleLeuThrIleThrMetLeuGlnPheLeu 187  
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Bunnayajola, metazoa; cinnuata; ciannata; vertebrae; euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

**AUTHORS**

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,

TITLE	JOURNAL	PUBMED	REFERENCE	AUTHORS
Gene trios	Science	302 (5652), 1960-1963 (2003)		
Interfing nonneutral evolution from human-chimp-mouse orthologous		14671302		
2 (bases 1 to 1770)				
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,				

**TITLE**  
JOURNAL  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Bethesda, MD 20814 USA

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 LOCUS AK080950  
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 ACCESSION AK080950  
 VERSION AK080950.1 GI:26348896  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Kono, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,  
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 TITLE RIKEN integrated sequence analysis (RISA) system-384-format  
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 Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076661

REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the  
 PANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 REFERENCE 5  
 AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 3171)  
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,  
 Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,  
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 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiko-cho, Tsukuba-shi, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/  
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US-10-626-445-8 (1-391) x AK080950 (1-3171)

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Qy      268 ----- 268
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Qy      268 ----- 268
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DEFINITION  
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ACCESSION  
BC018330  
VERSION  
BC018330.1 GI:17390772  
KEYWORDS  
HTC.  
SOURCE  
MUS musculus (house mouse)  
ORGANISM

REFERENCE  
AUTHORS  
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shellen, C.M., Schlier, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schenke, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ueda, T.B., Toshiyuki, S., Carninci, P., Prange, C., Kana, S.S., Loggellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McSwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hui, X., Gibbs, R.A., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butcherfield, Y.S., Krzywinski, M.I., Skaleja, U., Small, D.E., Scherker, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE 22388257 12479932

REFERENCE 2 (bases 1 to 1764)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov> Contact: MGC help desk Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov) Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC Web site: <http://www.hgsc.bcm.tmc.edu/cdna/> Contact: [amgdbcm.tmc.edu](mailto:amgdbcm.tmc.edu) Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louieged, H., Kovis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nananavati, A.N., Gibbs, R.A.

FEATURES SOURCE Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov> Series: TRAK Plate: 30 Row: m Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction, similarity but not identity to protein. This clone has the following problem: frame shifted.

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US-10-626-445-8 (1-391) x BC018330 (1-1764)

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LOCUS AK004891  
DEFINITION Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300003P04 product:ADRENERGIC RECEPTOR, ALPHA 1B, full insert sequence.





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 Qy 177 LeuThrIleMetLeuLeuGluPheLeuLeuPro-----ValIleSerValAlaTyr 194  
 Db 1122 GCCCTCTTTCCTCCCTGGGCTCTTTCATCATCCACCTGGCGGCTATCTCTGATGTAC 1181  
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 Qy 235 AlaCysArgThrSerAsnProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSer 254  
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 Qy 295 AlaGluLeuLeuArgGlyArgGlyLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314  
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 Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334  
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RESULT 13  
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 LOCUS AK043877  
 DEFINITION Mus musculus 10 days neonate cortex cDNA, RIKEN full-length  
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 ALPFA 1B, full insert sequence.  
 ACCESSION AK043877  
 VERSION AK043877.1 GI:26335985  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Mech. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 2  
 3 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes  
 MEDLINE Genome Res. 10 (10), 1617-1630 (2000)  
 PUBMED 20499374  
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 3  
 4 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,  
 Kono, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, Y.,  
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 TITLE RIKEN integrated sequence analysis (RISA) system-384-format  
 JOURNAL sequencing pipeline with 384 multicapillary sequencer  
 MEDLINE Genome Res. 10 (11), 1757-1771 (2000)  
 PUBMED 20530913  
 11076861  
 5  
 6 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 REFERENCE  
 1  
 2 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 GROUP Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation  
 JOURNAL of 60,770 full-length cDNAs  
 MEDLINE Nature 420, 563-573 (2002)  
 PUBMED 6 (bases 1 to 3050)  
 3 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,  
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 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N.,  
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shitaki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akehira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 TITLE Direct Submision  
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 Division of Experimental Animal Research in Riken contributed to  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail:genome-res@gs.c.riken.jp,  
 URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.jp/  
 URL:http://fantom.qualifiers

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REFERENCE 1 (bases 1 to 1203)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL PUBMED 14671302
REFERENCE 2 (bases 1 to 1203)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
TITLE

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